Sequence of c-erbB PKG-green fluoresc

fluorescent

Green

Amino acid sequenc

Human heregulin 2

Synthetic peptide E. coli RhtB prote Amino acid sequenc

C1C-K1 protein. R Human CLCNKB prote HaSNPV polypeptide

G-protein coupled G-protein coupled Numan PRO1415 (UNO N. mentngitidis se N. gonorrhoeae B h N. meningitidis se N. meningitidis se Human gene 16-enco

M2 region of volta Human secreted pro Human secreted pro Human secreted pro

Total number of

Database

Searched:

Scoring table: -Perfect score:

Sequence:

Title:

Run on:

Protein encoded by Human secreted pro Human secreted pro H. pylori GHPO 734 Antigen 2 from clu

numan secreted pro Polygalacturonase.

C. pneumoniae protH. pylori cytoplasHuman secreted pro

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antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIVI; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1; melanoma antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MKC class I molecule; major histocompatability complex; HIA-A2.1; 9mer; lOmer; anchor; human leukocyte antigen; PLP; 8mer; algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen fragment 1, from c-ERB2 has binding affinity for HLA-2.1.
                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grey HM, Kast WM, Sette A, Sidney J;
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W89879
Y34859
                           R39568
W85040
W85039
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                                                                                                                                                                                                                                                                                                                                                                                                              R73685 standard; peptide; 9 AA
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93US-0073205.
93US-0159184.
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                                                                   14-JUN-1995 (first entry)
                                                                                      herpes simplex virus
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                                                                   Homo sapiens
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R73685
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                    R73685
                                                                                                                                                                                                                                                                                                                                                                                                                        HER-2/new syntheti
HER-1/new protein
HER-2/new derived
HLA Class I motif
HLA class II bindi
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Her2-GM-CSF immuno
DC8scFv-erbB2EC fu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HER-2/neu protein.
                                                                               (without alignments)
20.233 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                   November 14, 2000, 11:54:42; Search time 15.21 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                       | SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                 268485 segs, 34193795 residues
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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W78859
W70057
Y10495
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R08222
W19764
Y44993
W01111
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W36824
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                      R73685-876 are potential peptide binders of HLA-A2.1 motif. Using motifs disclosed in the invention, these peptides were screened for further motifs. Only peptides with binding affinity of at least 1% (binding affinity is expressed as an IC50 value) as compared to the standard peptide (R71293) in assays. This peptide has an binding value of 0.1500. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R97507 is a peptide capable of activating cytotoxic T lymphocytes (CTLs) which specifically target malignant cells. The peptide corresponds to amino acids 369-377 of human Her-2/Neu protein. CTL-activating peptides can be used in a vaccine for protecting against tumour cell formation. CTLs activated by the peptides will lyse tumour cells displaying specific peptides. Antibodies against CTL-activating peptides are useful for the identification of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vivo activation of tumour-specific cytotoxic T lymphocytes - by contacting with polypeptide(s) derived from human p53 or Her-2/Neu
                                                                   Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; malignant cell; antigenic; vaccine; immunisation; activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 15;
Pred. No. 2.1e+05;
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                                                                                                                                                                             Disclosure; Page 80; 138pp; English
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                WPI; 1994-302678/37
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Synthetic peptides W36824-40 are based on the sequence of the human Her-2/neu protein, wherein each sequence contains the anchor motif for man leukocyte antigen (HLA) A2.1. The present peptide 1s based on positions 369-377. The ability of these peptides to inhibit the binding of an influenza virus matrix protein peptide M1 to HLA A2.1 was measured by inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic T lymphocyte (CTL) clone. The present protein showed 38% inhibition. The peptides were also tested for their ability to elicit an immune rosponse this will always to the tested for their and M7 (W36826) were able to do this. H3 and H7 peptides are tumour-associated antigens, and were used to immunize a transgenic, non-human vertebrate (that has been modified to express at least one HLA antigen), so that the annal protein the contains th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Her-2/neu protein; human leukocyte antigen A2.1; HLA;
cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;
T-cell receptor; TCR; tumour treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         manner. Cells expressing recombinant TCR are used to identify antigens associated with a tumour and to treat tumours in humans. Transgenic mice are a more convenient source of CTL than the tumour-infiltrating lymphocytes previously used. TCR can be humanised to reduce
similar compounds which may be useful for treating cancer or virally-infected cells, or for diagnosis. The peptide and vaccines produced provide immunity to a high percentage of different ethnic groups, i.e. those with different HIA alleles.
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding variable regions of HLA-restricted non-human \tau cell receptor specific for tumour antigen - used to identify tumour antigens and for tumour therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chains of such TCRs can be amplified from CTLs produced in the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              displays HLA-restricted T-cell receptor (TCR) specificity for the antigen. Nucleic acid encoding variable regions of the alpha and b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic peptide H3 based on the human Her-2/neu protein.
                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                     100.0%; Score 43; DB 17;
100.0%; Pred. No. 2.1e+05;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                            Sequence
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microparticle preparation (MP) has been developed, consisting of microparticles having a diameter of less than 100 mu m. The MP comprises:

(a) a polymeric matrix (PM) consisting of one or more synthetic polymers to a botymeric matrix (PM) consisting of one or more synthetic polymers consisting a solubility in water of less that 1 mg/1; and (b) an expression vector selected from RNA molecules (at least 50% of which are closed circles) or circular plasmid DNA (at least 50% of which are supercoiled).

Also described is a MP of at most 20 microns in diameter, comprising: (a) can PW: and (b) a NAM comprising an expression control sequence operatively linked to a coding sequence, where the coding sequence encodes an captession product selected from: (1) a polypeptide at least 7 amino cacids in length, having a sequence identical to the sequence of: (1) a fragment of a naturally-occurring mammalian protein: or (ii) a fragment of a naturally-occurring alength and sequence which permits it to cameman; (2) a peptide having a length and sequence which permits it to bind to an MHC class I or II molecule; and (3) the polypeptide or the peptide linked to a trafficking sequence. W69763 to W69765, and W78793 cow W78879 are peptide fragments for use in the present invention. The CMPS are highly effective vehicles for the delivery of polynucleotides incompany of polynucleotides incompany of permits in the present incompany of car incompany of the captering of the captering sequence. The time of the captering of
                                                                                                                                                                                                                       Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen; class II associated peptide; pathogen; gene therapy; genetic disease; infection; downregulation; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New preparations of microparticles - comprising a synthetic polymer matrix and nucleic acid comprising an expression vector for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 43; DB 19; Similarity 100.0%; Pred. No. 2.1e+05; 9; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Langer RS,
                                                                                                                                                                         HER-1/neu protein fragment 369-377.
                           W78859 standard; peptide; 9 AA.
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97US-0787547
                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Curley JM, Hedley ML,
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                                                                                                                            17-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide epitope W77119-W77138 were created for human tumour-specific cytotoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific timunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
side-reactions and short peptide derivatives of TCR are more economical to produce than TCR itself, particularly when expressed as a single-chain molecule rather than as a dimer.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disease specific immunogen - comprises disease specific cytotoxic T lymphocyte epitope used to elicit melanoma specific CTL response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                       100.0%; Score 43; DB 18; 100.0%; Pred. No. 2.1e+05;
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                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hunt DF, Kittlesen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HER-2/neu synthetic peptide epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olsclosure; Page 27; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VIRGINIA PATENT FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         W77131 standard; peptide; 9 AA.
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                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9833810-A2
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cytotoxic T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing a cytotoxic T lymphocyte response - by maintaining a level of antigen in the lymphatic system of a mammal so as to provide a sustained CTL response, used to treat, e.g. AIDS
                                                                                                                                                                                                                                                      Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 43; DB 20;
100.0%; Pred. No. 2.1e+05;
11ve 0; Mismatches 0;
                                                                                                                                                                                                  HLA Class I motif peptide SEQ ID NO:425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 43; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CTLI-) CTL IMMUNOTHERAPIES CORP.
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      Y10495 standard; Peptide; 9 AA.
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                                                                                                                                   12-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuendig TM, Simard JJL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-120514/10.
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Matches 9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KIFGSLAFL
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9902183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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      p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences shown in W70053 to W70075 represent peptides derived from HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte antigen (HLA), HLA-A1. and are used to axemplify the method of invention of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (HHC) molecules with antigen presenting cells (APC) pretreated with presence of at least 2 incubating the APCs with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytocxic T cells with APCs pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLs which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLs can be used for treating cancers, immune disorders, viral infections, the contains or the contacted infection, fungal infection, malaria or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                      Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of antigen-specific cytotoxic T cells - by incubating immunosent peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen presenting cells
                                                                                                                                                                                        HER-2/neu derived HLA-A2.1 binding peptide 5 (residues 369-377).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                    fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 77; 104pp; English.
W70057 standard; peptide; 9 AA.
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                                                                                                                             22-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9833888-A1.
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Gaps

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Sequence

RESULT Y10495 ,si

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Length 9; Indels

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Extracellular portion of the human epidermal growth factor receptor 2.
                                                                                                       Human epidermal growth factor receptor 2; HER2; vaccine; cancer.
                                              06-MAR-1991
                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1990;
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                 R08222;
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    The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an explosed from those represented by peptides Y98812-799339 which are derived from those representative by peptides Y98812-799339 which are derived from various antigens of the world wide population. The class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The peptide contained at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical focuses the immune response than or equal to 1,000 nM. The pharmaceutical focuses the immune response contained therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune containing the peptides of diseases that can be created using the peptide epitopes. Jyme disease, hepatitis, construction allorgists, lyme disease, hepatitis, construction and produced diseases which can be treated using immunogens administered with the peptides prostate cancer, hepatitis by hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condytoma acuminatum. The peptides may also be useful as diagnostic or therapeutic agents. The peptides may also be useful as diagnostic conserved to make monoclonal antibodies useful as potential diagnostic conserved to make monoclonal antibodies useful as petides may be used to predict which the readents. for example, to determine the susceptibility of an individuals will be at substantial risk of developing chronic infection. The selection of appropriater T and B cell epitopes should allow the conserved epitopes of pathogens which are characterized by high sequence conserved epitopes and malaria.
                           Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical; immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allorgy; lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.
                                                                                                                                                                                                                                                                                                                                                          compositions containing immunogenic peptide epitopes for various class II DR molecules useful for inducing helper T cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 21; Length 15; Pred. No. 0.009; 0; Mismatches 0; Indels
HLA class II binding antigen epitope peptide #35.
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 40; 60pp; English
                                                                                                                                                                                                                                                                                                   Sidney
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100.0%;
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                                                                                                                                                                                                                                                                                                   Southwood S,
                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                              WPI; 2000-097143/08.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                WO9961916-A1
                                                                                                                                                                                                          28-MAY-1999;
                                                                                                                                                                                                                                        29-MAY-1998;
                                                                                                                                                                             02-DEC-1999
                                                                                                                                                                                                                                                                                                   Sette A,
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note-327..353 /label= epitope "note= "potential T-cell epitope"

/label= epitope /note= "potential T-cell

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"potential T-cell epitope"

/label= epitope

/note=

197

T-cell epitope"

/label= epitope /note= "potential

113..130

/label= epitope /note= "potential T-cell epitope"

/label= epitope /note= "potential T-cell epitope"

'note= "potential T-cell epitope'

Location/Qualifiers

(first entry)

22..32 /label- epitope

/label= epitope /note= "potential T-cell epitope"

/note= "potential T-cell epitope"

/label- epitope

529

90WO-US02697.

/label= epitope /note= "potential T-cell epitope"

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HER2 extracellular domain used as vaccine - comprises sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    portions of the HER2 mol. The protein is antigenic in animals. Fragment comprising at least 9 amino acids open several possibilities for further research and a broad range of potential therapeutic apilications, e.g. for the treatment of mammmary gland adenocarcinoma and other cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This claimed sequence is free of transmembrane or intracellular
                                                                                                                                                                                                                                                                                                                                                                                                        at least 9 amino acid(s) prepd. using expression vector of DNA isolated from human epidermal growth factor receptor
                                                                                                                                                                Ullrich A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 13; 49pp; English.
89US-0354319
                                                                                                                                                                Hudziak RM, Shepard HM,
                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                            WPI; 1990-375946/50.
N-PSDB; Q06828.
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Gaps

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Conservative

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624 AA;

Sequence

R08222 standard; protein; 624 AA.

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RESULT R08222

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Kufer P, Dreier T,
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                           5
              1 KIFGSLAFL
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                                                                                                                                                                                                                                                                              Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                       Y44993;
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                                                                        RESULT 11
                                                                                    ¥44993
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              οy
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                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A fusion protein (W19764) comprises Her2 (a growth factor receptor that is overexpressed in breast, ovarian can other cancer cells) and granulocyte-macrophage colony stimulating factor (GM-CSF). It is the expression product of a nucleic acid molecule (T72755) prepd. by PCR amplification of Her2 cDNA from a breast cancer cell line and fusion to GM-CSF cDNA. Fusion expression vectors can be used to transfect mammallan and insect cells. The Her2-CM-CSF fusion protein is used to generate anti-Her2 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen-presenting cells exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response in a
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                                                                                                                                                                                                                                          er2-GM-CSF; granulocyte macrophage colony stimulating factor;
rowth factor receptor; oncogene; immunostimulant; cancer;
             DB 11; Length 624;
                                     Indels
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0
             Score 43; DB 1
Pred. No. 0.4;
Mismatches
                                                                                                                                                                                                                  Her2-GM-CSF immunostimulant fusion protein.
                                                                                                                                                                                                                                                                                                                 Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ACTI-) ACTIVATED CELL THERAPY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 8; 45pp; English.
                                                                                                                                           W19764 standard; Protein; 782 AA.
                                                                                                                                                                                                                                                                                                                                                   654..655
/label= Linker
656..782
/label= GM-CSF
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0
            100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                         /label- Her2
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                                                                                                                                                                                           (first entry)
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Query Match
Best Local Similarity
'... 9; Conserv?
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N-PSDB; T72725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vertebrate subject
                                                                        1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein.
                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                          Her2-GM-CSF;
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Protein
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Gaps

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100.0%; Score 43; DB 18; Length 782; 100.0%; Pred. No. 0.51; ive 0; Mismatches 0; Indels

Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative

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The patent discloses heterominibodies which are multifunctional compounds produceable in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains comprises, a CHI-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise,
                                                                                                              DC8 scrv; single-chain variable fragment; erbB2EC; extracellular domain; human; fusion construct; tetramerisation domain; constant domain; heterominbody; multifunctional compound; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; antiproliferative; prevention; treatment; malignant; haematopoletic cell; lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis \,
                                                                                     DC8scFv-erbB2EC fusion protein containing tetramerisation domain.
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "5' end of human IgG3 upper hinge region with additional residues"
                                                                                                                                                                                                                                                                                                       20..127
/label- DC8scFv_light_chain_variable_region
                                                                                                                                                                                                                                                                                                                                                                                DC8scFv_heavy_chain_variable_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zettl F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human_p53_tetramerisation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baeuerle PA, Borschert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
                                                                                                                                                                                                                                                                                                                                      128.142
/label- Glycine-Serine-linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Short_peptide_1.inker
                                                                                                                                                                                                                                                                                           'label - Leader_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erbB2EC_domain
                                                                                                                                                                                                                                                                  Location/Qualifiers
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Y44993 standard; Protein; 951 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            946..951
/label= His_tag
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                                                        23-MAY-2000 (first entry)
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/label= DC
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/label- er
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                                                                                                                                                                                                                                                                                                                                                                                                256..266
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/label=
                                                                                                                                                                                                                    - Unidentified.
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                                                                                                                                                                   Sequence
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   W92406;
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fused to the constant domains at least two (poly)peptides having different receptor or ilgand functions, where further at least two of the different (poly)peptides lack an intrinsic affinity for one another and are linked via the constant domains. The heterominibodies have cytostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.
                                                                                                                                The present sequence is a fusion protein comprising DC8 single-chain FV (scFV) fragment at the N-terminus, extracellular domain of human erbB2 at the C-terminus and a tetramerisation of main erbB2 at the C-terminus and a tetramerisation on an interpretation domain characterised in bacterial expression system is applicable for expression of fully functional and secretable recombinant protein in mammalian host cells. This tetrameric construct was not expressed as secretable and fully functional protein in mammalian cells. Hence general applicability of the tetramerisation domain for oligomerisation strategies in mammalian cells was ruled out.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/label- Intracellular_domain
/note- "claimed domain, useful for immunisation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding HER-2-new poly:peptide(s) - used for prevention or treatment of malignancies with which the HER-2/new oncogene is associated
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                                                                                                                                                                                                                                                                                                                                        100.0%; Score 43; DB 21; Length 951; 100.0%; Pred. No. 0.62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W01111 standard; Protein; 1255 AA.
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100...
See 9; Conservative
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N-PSDB; T40739.
                                                                                                                                                                                                                                                                                                                                                                                                                951 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 1 KIFGSLAFL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                       Gaps
Human HER-2/neu protein (W01111), also called p185 or c-erbb2, is the product of the HER-2/neo oncogene (see also 740739). The protein is over-expressed in various cancers, including breast, over-expressed in various cancers, including breast, over-expressed in various cancers, including breast, protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
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malignancy; treatment; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of HER-2/neu polypeptides - for eliciting an immune response an HER-2/neu associated malignancy, particularly for treating or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
676..1255
/note= "region which elicits immune response"
                                                                                                                                                                                                                                                    DB 17; Length 1255;
                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                    0.83;
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                                                                                                                                                                                                                                                100.0%; Score 43;
100.0%; Pred. No. C
Live 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          W92406 standard; Protein; 1255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human HER-2/neu oncogene protein.
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93US-0033644.
93US-0106112.
95US-0414417.
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N-PSDB; X01912.
                                                                                                                                                                                           1255 AA;
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Matches 9; Conserv
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Y84780;

RESULT 14 Y84780

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Heregulin 2; Her2; vaccination: cytotoxic T-lymphocyte immunity;
self-protein; cancer; breast cancer; prostate cancer;
cell-associated peptide antigen; foreign epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- insertion_region
/note= "suitable for foreign epitope insertion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label = insertion_region
/note = "suitable for foreign epitope insertion"
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/label- insertion_region
/note= "suitable for foreign epitope insertion"
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/label= insertion_region
/note= "suitable for foreign epitope insertion"
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/label- insertion_region
/note= "suitable for foreign epitope insertion"
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/label= insertion_region
/note= "suitable for foreign epitope insertion"
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/label= insertion_region
/note= "suitable for foreign epitope insertion"
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/label- insertion_region
/note- "suitable for foreign epitope insertion"
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/note "suitable for foreign epitope insertion"
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/label= insertion_region
/note= "sultable for foreign epitope insertion"
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/note- "suitable for foreign epitope insertion"
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210..224
/note= "sultable for foreign epitope insertion"
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/note= "sultable for foreign epitope insertion"
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/label- Ligand_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label - Cysteine_rich_domain
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                                                                                                                                                                                                                                                                                                                                                                     'note= "mature polypeptide"
                                                                                                                                                                                                                                                                                                                    .ocation/Qualifiers
                                                                               Y92620 standard; Protein; 1255 AA.
                                                                                                                                                                                                                                                                                                                                                   /label- N-terminal
                                                                                                                                                   (first entry)
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                                                                                                                                                                                  Human heregulin 2 (Her2).
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/label= C
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369 kifgslafl 377
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                 10-AUG-2000
                                                                                                                Y92620;
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents protein may be used to detect SPLICE erbB-2 in a sample. Agents protein may be used to detect SPLICE erbB-2 in a sample. Agents sPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the central nervous system and wound healing.
                                                                                                                                                                                                                                                                                                                                                                               SPLICE erbB-2 receptor protein; cell transformation disorder; cancer; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder;
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
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                                                            Score 43; DB 20; Length 1255; Pred. No. 0.83; 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 43; DB 21; Length 1255; Best Local Similarity 100.0%; Pred. No. 0.83; Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of the SPLICE erbB-2 receptor protein.
                                                                                                                                                                                                                                               Y84780 standard; Protein; 1255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 2; 60pp; English.
                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0165192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-CA00912.
                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muller WJ, Siegel PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-303768/26.
             1255 AA;
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                                                                                                                                                 11111111
369 kifgslafl 377
                                                                                                                              1 KIFGSLAFL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200020579-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     wound healing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-0CT-1998;
                                                                                                                                                                                                                                                                                                                 08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-2000
             Sequence
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Her2 can be used in the claimed method as an autovaccine to induce a CTL Her2 can be used in the claimed method as an autovaccine to induce a CTL Her2 can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfiable bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign T complete epitopes were identified (see features table). The method complete method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PSM) such as those associated with concers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simulateneous presentation by antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simulateneous presentation by antigen compression of the animal immune system of: (1) at least 1 compression from the cell-associated PA; and (2) at least 1 compact of all group which is foreign to the animal. Analogues of first T helper cell group which is foreign to the animal. Analogues of first T helper cell group which is foreign to the animal associated comprising a substantial cart of all known and predicted cyt and becall epitopes of the respective companies to breast cancer when the Da is human beta by human personate of producted cyteled prostate, prostate chreat prostate, and human personate of the pass to the respective companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
Gautam A, Birk P, Karlsson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
/label- insertion_region
/note- "suitable for foreign epitope insertion"
710..73
/label- insertion_region
/note- "suitable for foreign epitope insertion"
1011..1235
/label- C-terminal_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98DK-0001261.
98US-0105011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-DK00525.
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20-OCT-1998;
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100.0%; Score 43; DB 21; Length 1255; 100.0%; Pred. No. 0.83; 0; Indels 0; Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative 11111111 369 kifgslafl 377 1 KIFGSLAFL 9 ó

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Gaps

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Search completed: November 14, 2000, 11:55:20 Job tlme:  $38\ \mathrm{sec}$ 

## (OT92U) NIMA 18 30A9 SIHT

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APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
                      Sequence 2, Appli
Sequence 3, Appli
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 31, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
                                                                                                                                                                                                                                                                Sequence 12, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
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US-08-326-670A-2
US-08-537-361E-2
US-08-467-083-36
US-08-467-083-36
US-08-414-417B-36
US-08-486-348A-36
US-08-466-680B-36
US-08-466-680B-36
US-08-461-690B-21
US-08-461-690B-21
US-08-75-270A-12
US-08-75-270A-12
US-08-233-389C-1
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US-08-486-596A-1
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REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPA: 3723836 SEDANBERRY
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         US-09-004-713-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/08467083 Patent No. 5726023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Best Local Similarity 100.
Matches 9; Conservative
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TYPE: amino acid
STRANDEDNESS:
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124
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     Search time 12.27 Seconds (without alignments)
12.294 Million cell updates/sec
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Sequence 27,
Sequence 10,
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Sequence 70,
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: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
: /cgn2_6/ptodata/2/laa/6_COMB.pep:*
: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                           4.5
Compugen Ltd
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US-08-787-547-70

US-08-486-3488-27

US-08-486-5458-27

US-08-902-516-18

US-08-466-6808-27

US-08-466-6808-62

US-08-466-6808-62

US-08-466-6808-62

US-08-466-6808-62

US-08-466-6808-62

US-08-466-6808-62

US-08-466-6808-68

US-08-467-083-68

US-08-414-4178-68

US-08-414-4178-68

US-08-467-083-68

US-08-486-3488-68

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US-08-466-6808-68

US-08-378-36-786-2

US-08-378-36-786-2

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US-08-378-36-786-2

US-08-378-36-786-2

US-08-378-36-786-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   164575 seqs, 16761186 residues
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                           GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                     November 14, 2000, 11:54:42
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                      - protein search, using
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seq length: 2000000000
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Maximum DB
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Sequence 27, Application US/08486348A

Patent No. 5846538

GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: FOR DIAGNOSTS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69 - CONFESSIONDENCE Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-MAR-1995
                     6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CALLCATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 43; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/ACENT INPORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REPERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISB PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 amino acids
      Abu...
STREET: bo..
CITY: Seattle
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Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
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                                                                                                   98104-7092
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US-08-414-417B-27
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Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
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                                                                                                                                      Sequence 70, Application US/08787547

Patent No. 5783567

GENERAL INFORMATION:

APPLICANT: Curley, Joanne M.

APPLICANT: Curley, Joanne M.

APPLICANT: Langer, Robert S.

TITLE OF INVENTION: OF NUCLEIC ACID

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows95
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILLING DATE: 22-JAN.1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0819
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Fraser, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-787-547-70
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1 KIFGSLAFL 9
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                         1 KIFGSLAFL 9
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CITY: Boston
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US-08-787-547-70
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Gaps ö

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APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE S: ADDRESS: ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                         William MEMBANE-BOUND CYTOKINE COMPOSITIONS COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE RESPONSE USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
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Sequence 18, Application US/08902516
Patent No. 5891432
GENERAL INFORMATION:
APPLICANT: Soo Hoo, William
TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF TITLE OF INVENTION: RESPONSE USING SAME COMPOSED: CORRESPONDERCE S 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
COUNTRY: United States.
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 27, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (619)535-9001
(619)535-8949
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: peptide
US-08-902-516-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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APPLICANT: Cheever, Martin A.

APPLICANT: Cheever, Mary L.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

CORRESPONDENCE Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 32,629
RECISTRATION NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                   100.0%; Score 43; DB 2; I
100.0%; Pred. No. 1.2e+05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/08468545B Patent No. 5876712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino 27: The sequence characteristics:
  TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Washington
COUNTRY: US
ZIP: 98104-7092
                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                    1 KIFGSLAFL 9
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US-08-486-348A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-468-545B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-468-545B-27
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Sequence 62, Application US/08467083
Sequence 62, Application US/08467083
Sequence 62, Application US/08467083
Sequence 62, Application US/08467083
Sequence 62, Application Sequence 63, Applicant Cheever, Martin A. APPLICANT: Disis, Mary L. APPLICANT: Disis, Mary L. TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN TITLE OF INVENTION: HBR-2/NEU ONCOGENE IS ASSOCIATED NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Derry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/08414417B
Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/414,417
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 622-4900
TELEFAN: (206) 622-4901
TELEFAN: (206) 622-4901
TELEFAN: (206) 622-6031
TELEFAN: (206) 622-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                           Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
                                         9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
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                                                                                   1 KIFGSLAFL 9
                                                                                                         Seattle
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US-08-414-4178-62
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US-08-467-083-62
                                                                                                                                                                                                           US-08-467-083-62
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                                         Matches
                                                                                                                                                                                          RESULT
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Sequence 10, Application PC/TUS9516415

GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
TITLE OF INVENTION: CYTOTOXIC T CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16415
FILING DATE: 13-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 4;
Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 3;
Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 North Torrey Pines Road, TPC-8
                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPATION (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
06-JUN-1995
06-JUN-1995
18. 424
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,558
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOGBN, APril C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 433.1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-6312
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                          LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
                                   APPLICATION NUMBER:
FILING DATE: 06-JUN
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 10666 North
CITY: La Jolla
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KIFGSLAFL 9
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US-08-466-680B-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
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APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
ATITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 43; DB 2; Length 16; Best Local Similarity 100.0%; Pred. No. 0.0076; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application US/08468545B
Patent No. 5876712
GENERAL INFORMATION:
       INFORMATIONE: (206) 62-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
STRANDEDNESS:
TOPOTIONE
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-486-348A-62
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ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                             1 KIFGSLAFL 9
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Petent No. 5846538
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES:
ADDRESSEE: Seed and Berry LLP
STRREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-AAR-1995
CLASSIFICATION: 424
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SCFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/486,348A
FILING DATE: UN-3UN-1995
CLASSIFICATION: 424
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Flith Avenue
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/POCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READARDE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
NUMBER OF SEQUENCES:
                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS:
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ZIP: 98104-7092
                                                                                                                                COUNTRY: US
ZIP: 98104-7092
                                                                                         Seattle
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WinPatin (Genentech)
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
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NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Marches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650-324-0960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: Linear
US-08-422-108-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-146-283-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                            APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/Neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTEN READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 43; DB 3; Best Local Similarity 100.0%; Pred. No. 0.0076; Matches 9; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hudziak, Robert M.
APPLICANT: Shepard, H. Michael
APPLICANT: Ullrich, Axel
TITLE CANT: ULLRICH: HER2 EXTRACELLULAR DOMAIN
NUMBER OF SEQUENCES: .2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sharkey, Richard G.
RECISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SED ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/466,680B FILING DATE: 06-0UN-1995 CLASSIFICATION: 424
                                  Sequence 62, Application US/08466680B Patent No. 6075122
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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Patent No. 6015567
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 amino acids
                                                                                                                                                                                                                                                                STREET: 6300 COlumb
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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            US-08-466-680B-62
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Laus, Relner
APPLICANT: Laus, Relner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TTLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 43; DB 3;
100.0%; Pred. No. 0.33;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
FILING DATE: 14-Apr-1995
                                                                                                                                                                                                                                                                                                                                                                                        554C2D2
                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/355460
FILING DATE: 13-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/048346
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09146283
Patent No. 5976546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    NAME: Lee, Wendy M
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
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SEĞUENGTH: 782 amino acids
TYPE: amino acids
TOPOLOGY: 1inear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
US-09-146-283-4
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0; Gaps Ouery Match

100.0%; Score 43; DB 2; Length 782;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels

; 0

Search completed: November 14, 2000, 11:55:00 Job time: 18 sec

1 KIFGSLAFL 9 |||||||||| 369 KIFGSLAFL 377

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(OTARU) NIMAJA 30A9 SIIII

	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - pro	OM protein - protein search, using sw model
Run on:	November 14, 2000, 11:54:42; Search time 13.48 Seconds (without alignments) 42.370 Million cell updates/sec
Title	US-09-277-074-10
Sequence:	4.3 1 KIFGSLAFL 9
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

182106 segs, 63460219 residues

Searched:

182106

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su length: 0 length: 2000000000 sed Minimum DB s Maximum DB s

1: pir1:\* 2: pir2:\* 3: pir3:\* PIR\_65:\*

Database

pir4:\*

summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ribosomal protein hypothetical prote probable membrane hypothetical prote cytochrome B (EC 1 ubiquinol--cytochr probable olfactory hypothetical prote NADH dehydrogenase p-185 precursor -protein-tyrosine k protein-tyrosine k hypothetical prote conserved hypothet oligopeptide ABC t hypothetical prote hypothetical prote protein kinase (EC protein kinase (EC ORF MSV137 hypothe conserved hypothet hypothetical prote prote protein kinase (EC major facilitator probable membrane hypothetical 15.4 hypothetical hypothetical Description SUMMARIES T28747 S53849 T488578 T66215 T166215 F81954 F81954 F81011 S58038 T200547 T200540 OKBOG S05702 S62432 S56229 A65187 T28298 H69173 E72119 B72282 T20920 T33989 I48161 A24571 TVRTNU E7071 S72791 Query Match Length DB Score Result 

hypothetical prote	hypothetical prote	probable transport	chloride channel,	chloride channel C	chloride channel C	chloride channel C	centromere-binding	hypothetical prote	T16G12.5 protein -	TipC protein - sli	hypothetical prote	lipophorin - fruit	hypothetical prote	hypothetical prote
T28975 F71419	T26764	S60912	A45483	A57713	D57713	C57713	S64449	T32574	S42839	T17414	S76412	T13812	T07326	A72256
7 7	7	~	~	~	~	~	~	~	~	7	7	7	7	7
350	505	573	989	687	687	687	926	965	1483	3848	4199	3351	51	77
72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	70.9	69.8	69.8
31	31	31	31	31	31	31	31	31	31	31	31	30.5	30	30
0-	~	3	4	'n	G	7	œ	œ	_	_	~	9	<b>-</b>	10

## ALIGNMENTS

9 Y.; Ishika			; 0
RESULT 1 14816.1 16816.1 17 185 precursor - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Species: Mesocricetus auratus (golden hamster) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999 C;Accession: 148161 R;Nexamura, T; Ushilima, T; Ishizaka, Y; Naqao, M.; Arai, M.; Yamazaki, Y.; Ishika	Gene 140, 251-255, 1994 A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene. A;Reference number: 148161; MUID:94193007 A;Accession: 148161 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Rolecule type: mRNA A;Rolecule type: RRNA A;Rosidues: 1-1254 <res></res>	A;Cross-references: GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595 C;Genetios: A;Gene: neu C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Reywords: APP F;718-983/Domain: protein kinase homology <kin> F;718-987/Region: protein kinase ATP-binding motif</kin>	100.0%; Score 43; DB 2; Length 1254; Similarity 100.0%; Pred. No. 0.72; 9; Conservative 0; Mismatches 0; Indels 0; Gaps
RESULT 1 148161 p-185 precursor - 9 C;Species: Mesocric C;Date: 02-Jul-1996 C;Accession: 148161 R;NeKamura, T; Ush	Gene 140, 251-255, 19 A,Title: Cloning and A,Reference number: I A,Accession: I48161 A,Status: preliminary A,Molecule type: mRNA A,Residues: 1-1254 «RN	A; Cross-references C, Genetics: A; Genetics: C; Superfamily: epi C; Keywords: ATP F; 718 983/Domain: F; 726-734/Region:	Query Match Best Local Matches

369 KIFGSLAFL 377 1 KIFGSLAFL 9 ò

Accession: A24571 A25491 A24188; ECC 2.7.1.112) erbB2 precursor - human N.Alternate names: C-erb-B-2 protein precursor; Kinase-related transforming protein e. Species: Homo sapiens (man) C.5pecies: Homo sapiens (man)

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A:Gene: neu
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Superfamily: epidermal growth factor receptor; protein; phosphoprotein; phosphorylation; duplication; glycoprotein; phosphorotein; signal sequence *status predicted <SIG>
F:10-1260/Product: protein-tyrosine kinase neu *status predicted <MAT>
F:508-680/Domain: transmembrane *status predicted <TMN>
F:731-739/Region: protein kinase homology <KINN>
F:731-739/Region: protein kinase ATP-binding motif
F:71-191.263,535,576,634/Binding site: carbohydrate (Asn) (covalent) *status predicted
F:691/Binding site: phosphate (Thr) (covalent) *status predicted
F:882,1227,1253/Binding alte: phosphate (Tyr) (covalent) *status predicted
                                                                                                                                                                                                                        A; Molecule type: MRNA
A; Residues: 1-1260 CARN>
A; Residues: 1-1260 CARN>
A; Residues: 1-1260 CARN>
A; Residues: 1-1260 CARN>
A; Residues: EMBL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746
B; Masul, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohe Carcinogenesis 12, 1975-1978, 1991
A; Tile: Direct DNA sequencing of the rat neu oncogene transmembranc domain reveals n A; Reference number: A61204; MUID:92035293
A; Reference number: A61204
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Note: authors translated the codon GCA for residue 25 as Val
C; Genetics:
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999
C;Accossion: A24562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein
A;Reference number: A24562; MUID:86118662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross-references: EMBL: AF039044; PIDN: AAC47951.1; GSPDB:GN00023; CESP: F48G7.1
A; Experimental source: strain Bristol N2; clone F48G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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R; Clarke, K.; Wohldmann, P.; Harrlson, M.
submitted to the EMBL Data Library, January 1998
A; Description: The sequence of C. elegans cosmid F48G7.
A; Reference number: Z20517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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A;Introns: 64/3; 148/3; 220/1; 301/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.7%;
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Best Local Similarity
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                                                      A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, F
Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos
A;Reference number: A44188; MUID:86070181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: DNA
A Residuces: 812-999 kms.
A Residuces: 812-9995; NID:9459807; PIDN:AAA35809.1; PID:9459808
A Cross-references: GB:L29995; NID:9459807; PIDN:AAA35809.1; PID:9459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
R;Tal, M.; King, C.R.; Promore: 1987
A;Title: Human HER2 (neu) promores: evidence for multiple mechanisms for transcriptional
A;Reference number: 157622; MUID:87286898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP C; Superfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1.517, "RALL', 522, 'S', 524-654,'V', 656-1169,'A',1171-1255 <COU2>
A; Cross-treferences: GB:M11730; NID:9183986
R; King, C.R.; Kraus, M.H.; Aaronson, S.A.
Schence 229, 974-975, 1985
A; Title: Amplification of a novel v-erb8-related gene in a human mammary carcinoma.
A; Reference number: 159509; MUID:85272597
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A; Molecule type: DNA
A; Residues: 740-910 <COUI>
A; Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: GDB:120613; OMIM:164870
A:Map position: 17q21..17q21..1
A:Introns: 25/1; 75/3; 147/1; 883/3
A:Note: the list of introns is incomplete C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: I59509
A; Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 9; Conserv
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369 KIFGSLAFL 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m
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RESULT IVRTNU

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us-09-277-074-10.rpr

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Gaps

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79.1%; Score 34; DB 2; Length 370; 87.5%; Pred. No. 17; 1.1ve 0; Mismatches 1; Indels
submitted to the Protein Sequence Database, April 2000
A;Reference number: 224490
A;Recession: T48578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 < ABEV>
A;Cross-references: EMBL>A;Experimental source: cultivar Columbia; BAC clone 731B5
C;Genetics: A;Map position: 5
A;Introns: 119/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 KIFGSLPF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIFGSLAF 8
                                                                                                                                                                                                                                                                                                                       A; Note: T31B5.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
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                                                                                                          hypothetical protein PH1141 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: G71055
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamaanoto, S.; Sekin
M.; Ohituku, Y.; Funahabashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137
A;Reference number: A71000; MUID:98344137
A;Accession: G71055
A;Status: prealiminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-502 <AMA>
A;Residues: 1-502 <AMA>
A;Residues: 1-502 <AMA>
A;Cross-references: GB:AP000005; NID:93236132; PIDN:BAA30241.1; PID:93257558
A;Stors-references: CB:AP000005; NID:93236132; PIDN:BAA30241.1; PID:93257558
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1141
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein S3 - Acanthamoeba castellanii mitochondrion
C;Species: mitochondrion Acanthamoeba castellanii
C;Date: 15-Uul-1995 #sequence_revision 01-Sep-1995 #text_change 07-Dec-1999
C;Accession: 553849
B;Burger, G;;Plante, I;Lonergan, K.M.; Gray, M.W.
J. Mol. Biol. 245, 522-537, 1995
A;Title: The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba castellanii: comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 cBUR>
A:Residues: 1-298 cBUR>
A:Coss-references: GB:U12386; NID:9562028; PID:9562053
A:Experimental source: strain Neff; ATCC 30010
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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Pred. No. 8.5;
1; Mismatches
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Pred. No. 13;
0; Mismatches
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87.58;
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87.58;
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.1
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genetic code: SGC6
C; Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome: mitochondrion
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123 LFGSLAFL 130
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RESOLT 8

SEGIST 8

RESOLT 8

RESOLT 8

RESOLT 8

RESOLT 8

RESOLT 8

RATELER membrane protein RFL040w - yeast (Saccharomyces cerevisiae)

N.Alternate names: protein R004

C. Decession: Sc6125, S60496

C. Accession: S66125, S60496

R. Murakani, Y.; Natloo, M.; Sasanuma, S.1.; Sas submitted to the EMBL. Data inherary, May 1959

A. Accession: S66125, S60496

A. Accession: S66125, S60496

A. Accession: S66125, S60496

A. Accession: S66125, S60496

A. Moclecule type: DMA

A. Residues: 1-540 < MUPS

B. Residues: 1-540 < MUPS

F. 134-1340 main: transmembrane #status predicted < TMA>

F. 134-1340 main:
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llarity 87.5%; Pred. No. 24;
Conservative 0; Mismatches 1; Indels
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Gaps

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probable olfactory receptor tpcr21 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C;Accession: S58038
R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
R;Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
A;Description: Male germ cells from several mammalian species express a specific repe
                                                                                                                                                                                                               A;Cross-references: GB:AE002555; GB:AE002098; NID:g7227310; PIDN:AAF42372.1; PID:g722
A;Experimental source: serogroup B, strain MMD58
C;Genetics: NMD2052
A;Gene: NMD2052
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
A;Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 04-Mar-2000
C.Sceasion: T20847
R.Steward, C.
submitted to the EMBL Data Library, February 1996
A.Reference number: 219290
A.Rocession: T20847
A.Rocessi
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A; Residues 1.157 cVANA
A; Cross-references: EMBL:X89704; NID:g902724; PIDN:CAA61851.1; PID:g902725
C; Superfamily: olfactory receptor OR14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 4
A;Introns: 14/3; 47/3; 68/3; 123/3; 149/3; 179/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F07C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 157;
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85.7%; Pred. No. 19;
11ve 1; Mismatches
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Pred. No. 27;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB
Pred. No. 32;
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62.58;
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87.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.7
Best Local Similarity 87.5
Matches 7; Conservative
                                                                A; Accession: E81011
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-449 <TET>
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A; Status: preliminary
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| 127 FGSLAFM 133
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                                                                                                                                                              C. Accession: T1642

R.Miller, N.

Bubmitted to the EMBL Data Library, November 1995

A. Reference number: 218514

A. Reference number: 218514

A. Accession: T1642

A. Status: pre-liminary; translated from GB/EMBL/DDBJ

A. Residues: 1-120 < MILLS

A. Residues: 1-120 < MILLS

A. Cross-references: EMBL:U40953; NID:91072248; PID:91072249; PIDN:AAB52646.1; GSPDB:GNOG

C. Genetics:

C. Genetics:

C. Genetics:

C. Genetics:

C. Accession: T1642

A. Cross-references: EMBL:U40953; NID:91072248; PID:91072249; PIDN:AAB52646.1; GSPDB:GNOG

C. Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. Species: Neisseria meningitidis
C. Species: Neisseria meningitidis
C. Species: Neisseria meningitidis
C. Species: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C. Accession: F81954
R. Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, indroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
Nature 404, 502-506, 2000
A. Mattle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
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A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: DNA
A;Residues: 1-449 <PAR>
A;Cross-references: GB-AL162753; GB:AL157959; NID:g7379120; PIDN:CABB3685.1; PID:g737913
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: petB; NMA0384
C;Keywords: oxidoreductase
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0
                                                            hypothetical protein F53B1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
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Pred. No.
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87.58;
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87.58;
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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98 IFGSLLFL 105
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A; Introns: 48/2; 71/3
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A; Residues: 63-92, X', 94; X', 219-223, X', 225-227, XX', 230-255; 294-323 <FRA>
A; Residues: 63-92, X', 94; X', 219-223, X', 225-227, XX', 230-255; 294-323 <FRA>
C; Superfamily: cGMP-dependent protein Kinase; CAMP receptor protein cyclic nucleotide-bi
C; Keywords: acetylated amino end; alternative splicing; ATP; autophosphorylation; CGMP F; 118-235/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology (CRPI>F; 236-293/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology (fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A.Residues: 'E', 64-75 <WOL>
A.Residues: 'E', 64-75 <WOL>
A.Respelmental source: aortic smooth muscle
A.Rote: monomeric form apparently produced by proteolysis during purification
B.Francis, S.H.; Woodford, T.A.; Wolfe, L.; Corbin, J.D.
Second Messengers Phosphoproteins 12, 301-310, 1989
A.Title: Types Ialpha and Ibeta isozymes of cGMP-dependent protein kinase: alternative
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J. Balol. Chem. 264, 4157-4162, 1989
A:Title: Properties of a cGMP-dependent monomeric protein kinase from bovine andra.
A:Reference number: A32952; WUID:89139489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Cross-references: EMBL:X69067; NID:g505262; PIDN:CAA48818.1; PID:g578449
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
C:Genetics:
A:Gene: ND-1
                                                                                                                                                                                                          NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - brine shrimp mitochondrion
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C;Species: Bos primigenius taurus (cattle)
C;Species: 07-sep-1990 fsequence_revision 24-Feb-1995 #text_change 04-Feb-2000
C;Accession: S05035; A32952; A60180
R;Wernet, W.; Flockerzi, V.; Hoffmann, F.
FEBS Lett. 251, 191-196, 1989
A;Title: The CDNA of the two isoforms of bovine cGMP-dependent protein kinase. A;Reference number: S05034; MUID:89325663
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A;Residues: 1-293 <WER>
A;Cross-references: EMBL:X54289; NID:g213; PIDN:CAA38184.1; PID:g214
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Pred. No. 35;
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62.58;
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Best Local Similarity
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241 VFGSMSFL 248
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44 QVFGSIAF 51
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F;2/Modified site: acetylated amino end (Gly) (in mature form) *status predicted F;80/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) *status predic
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                      Gaps
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DB 2; Length 323;
38;
                      Indels
                     1; Mismatches
 Score 32;
Pred. No.
 74.48;
66.78;
Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Search completed: November 14, 2000, 11:55:59 Job time: 77 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

November 14, 2000, 11:54:42; Run on:

Search time 8.66 Seconds (without alignments) 33.202 Million cell updates/sec

US-09-277-074-10 Title: Perfect score: Sequence:

1 KIFGSLAFL 9

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

87993 seqs, 31947931 residues Searched:

87993 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	553 mes	$\sim$	1 rattu	•	P43562 saccharomyc	artem	80925 human papil	:4	13976 homo sapien	-		14619 homo sapien	9z0z0 mus musculu	09782 schizosacch	43571 saccharomyc	27847 escherichia	Q10647 mycobacteri	53426 mycobacteri		51804 oryctolagus	P51800 homo sapien	51803 oryctolagus	Q06393 rattus norv	51801 homo sapien				P97297 mus musculu	75424 mycoplasma	9	9	24305	39589 bacillus su
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SUMMARIES	QI	ERB2_MESAU	ERB2_HUMAN	ERB2_RAT	RT03_ACACA	YFEO_YEAST	NU1M_ARTSF	VL2_HPV48	KGPA_BOVIN	KGPA_HUMAN	KGPA_RABIT	KGPB_BOVIN	KGPB_HUMAN	KGPB_MOUSE	YA93_SCHPO	YFC5_YEAST	RHTB_ECOLI	YD37_MYCTU	YD37_MYCLE	ALP1_YEAST	CICL_RABIT	CICK_HUMAN	CICK_RABIT	CICK_RAT	CICL_HUMAN	CB31_YEAST	MSCL_STAAU	DIVC_BACSU	ADML_MOUSE	Y252_MYCPN	COX3_LEITA	UN97_CAEEL		YWBF_BACSU
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P38967 saccharomyc P07264 saccharomyc P56690 thermus agu		P399/9 saccharomyc P31526 synechococc O95169 homo saplen P31783 bos tautus	
TAT2_YEAST LEU2_YEAST SYI THETH	CHS2_YEAST EFG_PLARO CHCB_BOMMO	TEHO_TEAST YPS2_SYNP2 NIAM_HUMAN CD8A_BOVIN	ERMG_BACSH BEX1_HAEIN
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592 779 821	963 128 174	1, 3 1, 84 1, 86 2, 4, 2	244 265
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## ALIGNMENTS

Natl. Acad. Sci. U.S.A. 82:6497-6501(1985)

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                                                                                                                                                                                                           PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2 PRECURSOR (EC 2.7.1.112)
(P1895RBB2) (NEU PROTO-ONCGENE) (C-ERBB-2) (TYROSINE KINASE-TYPE CELL SURFACE RECEPTOR HER2) (MLN 19).
ERBB2 OR HER2 OR NGL OR NEU.
                       ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 86016729.
Semba K., Kamata N., Toyoshima K., Yamamoto T.;
Semba K., Kamata N., Toyoshima K., Yamamoto T.;
A. v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a human salivary gland adenocarcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE; 86118663.
Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Francke U., Levinson A., Ullrich A.; "Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with new oncogene.";
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo
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"Similarity of protein encoded by the human c-erb-B-2 gene epidermal growth factor receptor.";
Nature 319:230-234(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J., Francke U., Levinson A., Ullrich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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974C3791C21F2BE1 CRC64;
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V -> E (IN ONCOGENIC NEU).
                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                     PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Disease mutation
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Similarity 100.0%;
9; Conservative 0;
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Best Local Similarity
Matches 9; Conserv
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369 KIFGSLAFL 377
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 Proto-oncogene;
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ID ERB2_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        RESIDUES (BY SIMILARITY).

-!- POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POLYMORPHISM: THERE ARE FOURS ALLELE B1 (654-LLE-LLE-655) HAS A FREQUENCY OF 0.782: ALLELE B2 (654-LLE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

HOSPHORYLATION (AUTO-) (BY SIMILARITY).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                            Ebsani A., Low J., Wallace R.B., Wu A.M.; "Characterization of a new allele of the human ERBB2 gene by allele-specific competition hybridization."; Genomics 15:426-429(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DON; 1.
PROSITE; PS50011; PROTEIN_KINASE_DON; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                    -i- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGE, TGF-ALPHA AND AMPHIREGULIN.

-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                        PROTEIN TYROSINE PHOSPHATE.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).
                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M11762; AAA35808 1; JOINED.
EMBL; M11762; AAA35808 1; JOINED.
EMBL; M11763; AAA35808 1; JOINED.
EMBL; M11765; AAA35808 1; JOINED.
EMBL; M11765; AAA35808 1; JOINED.
EMBL; M11706; AAA35808 1; JOINED.
EMBL; M12036; AAA35978 1; EMBL; X03363; CAA27060.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPR000494; ...
INTERPRO; IPR001245; ...
INTERPRO; IPR001245; ...
INTERPRO; IPR002174; ...
PFAM; PF00757; Furin-like; 1.
PFAM; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M11767; AAA35808.1; -.
EMBL; M11761; AAA35808.1; JOINED.
                                 AND VAL-655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pkinase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A25491; A25491.
PIR; A24571; A24571.
HSSP; P11362; 1FGI.
MIM; 164870; -.
                                 VARIANTS VAL-654 AN MEDLINE; 93194196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism.
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MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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BINDING
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SEQUENCE FROM N.A.
STRAIN-ATCC 30010 / NEFF;
MEDLINE; 95147275.
Burger G., Plante I., Lonergan K.M., Gray M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAXY-2000 (Rel. 39, Last annotation update)
MITOCHONDRIAL RIBOSOMAL PROTEIN 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Acanthamoebidae; Acanthamoeba
                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                         CYS-RICH
                                                                                                               HSSP, P11362; IFGI.
INTERPRO; IPR000494; -.
INTERPRO; IPR0007199; -.
INTERPRO; IPR001245; -.
INTERPRO; IPR002145; -.
PFAM, PF00757; Furin-like; 1.
PFAM; PF001030; Recep_L_domain; 2.
PFAM; PF001030; Recep_L_domain; 2.
                                                                                          EMBL; X03362; CAA27059.1; ALT_INIT.
PIR; A24562; TVRTNU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         castellanii (Amoeba).
                                                                                                                                                                                                                                                                     Proto-oncogene; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138831
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1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acanthamoeba
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P46754;
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BINDING
ACT_SITE
VARIANT
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MOD_RES
CARBOHYD
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TRANSMEM
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A Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,

A MEDLINE; 92155181.

A Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,

A Crumpton M.J., Sternberg M.J.E., Campbell I.D.;

Oncogenic and oncogenic forms of the new protein.";

EMBO J. 11:43-48[1992].

11:43-48[1992].

12: FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,

ALPHA AND AMHIREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A

POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-

ALPHA AND AMHIREGULIN.

C. 1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

PROTEIN TYROSINE PHOSPHATE.

THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.

THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.

C. 1- SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.

C. 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 86118662.
Bargmann C.I., Hung M.-C., Weinberg R.A.;
"The neu oncogene encodes an epidermal growth factor receptor-related
protein.";
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                          ERB2_RAT STANDARD; PRT; 1257 AA.
P06494;
01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112)
RELATED PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extended family of protein-tyrosine kinase genes differentially
                       (POTENTIAL).
   (POTENTIAL)
              (POTENTIAL)
                                               (POTENTIAL)
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                                                                                                                                                  100.0%; Score 43; DB 1; Length 1255; 100.0%; Pred. No. 0.39;
                                                                                                     -> A (IN REF. 2).
39E9DFDA04DCF962 CRC64;
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                         ö
N-LINKED (GLCNAC. .
I -> V.
/FTIG=VAR_004077.
                                                                                I -> V. //FTId=VAR_004078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                                                                                                                                                          Mismatches
                                                                                                                 137909 MW;
                                                                                                                                                                         ö
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                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 319:226-230(1986)
 187
259
530
571
629
654
                                                                                                      1170
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-NEUROBLASTOMA;
                                                                                                               1255 AA;
                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                            369 KIFGSLAFL 377
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                                                                                                                                                                                                1 KIFGSLAFL
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKED (GLCNAC. . .) (POTI 6129264583011402 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYS-RICH.
PROTEIN KIRASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Hypothetical
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037714;
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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                      J. Mol. Biol. 245:522-537(1995).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995)
-!- SUBCELUULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                         ;
0
"The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE; 95400292.
MURSMAIN Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                            79.1%; Score 34; DB 1; Length 298; 87.5%; Pred. No. 7.3; 1:ve 0; Mismatches 1; Indels
              complete sequence, gene content and genome
                                                                                                                                                                                                                            PEAM: PF00189; Ribosomal_S3_C; 1.
PFAM: PF00417; Ribosomal_S3_N; 1.
PROSITE; PS00548; RIBOSOMAL_S3; FALSE_NEG.
Ribosomal protein: Mitochondrion.
SEQUENCE 298 AA; 36060 MW; 29415935EE187DE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD: SO001854: YFL040W.
INTERPRO: IPR001066: -
PFAM: PF00083: sugar_Lr: 1.
PROSITE: PS00216: SUGAR_TRANSPORT_1: FALSE_NEG.
PROSITE: PS00217: SUGAR_TRANSPORT_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PROBABLE METABOLITE TRANSPORT PROTEIN YEL040W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                      EMBL; U12386; AAD11841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D50617; BAA09200.1; -. EMBL; D44598; BAA08025.1; -.
                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 87.3.
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250 KAFGSLAF 257
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                          organization.";
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P43562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
Mitochondrion.
                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 540;
Pred. No. 13;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.4%; Score 32; DB 1; Length 298; ilarity 62.5%; Pred. No. 19; Conservative 3; Mismatches 0; Indels
   Transmembrane.
                                                                                                                                                                                                                                             A43B6B58134C38AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AA
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                                    POTENTIAL.
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PROSITE; PS00667; COMPLEXI_NDI_1; 1.
PROSITE; PS00668; COMPLEXI_NDI_2; 1.
                                                                                                                                                                                                                                             Ψ.,
     Repeat;
                                                                                                                                                                                                                                                                                                 79.1%;
87.5%;
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60610 P
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                     protein;
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 94223692.
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Best Local Similarity
Matches 5; Conserv
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241 VFGSMSFL 248
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MEDLINE; 82098123
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INIT_MET
0
MOD_RES
1
DISULFID
42
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SEQUENCE
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DOMAIN
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                         Human papillomavirus type 48.
Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1
ALPHA) (CGKI-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 85023307.

Takio K., Wade R.D., Smith S.B., Krebs E.G., Walsh K.A., Titani K.; Ganosinne cyclic 3',5'-phosphate dependent protein kinase, a chimeric protein homologous with two separate protein families."; Blochemistry 23:4207-4218(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wernet W., Flockerzi V., Hofmann F.; "The cDNA of the two isoforms of bovine cGMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                ;;
                                                                                                                                                                                                                                                                                                                                                           Length 502;
                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 83213511.
Takio K., Smith S.B., Walsh K.A., Krebs E.G., Titani K.;
                                                                                                                                                                Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         502 AA; 54435 MW; C42DE45A7E73EE29 CRC64;
                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1;
Pred. No. 32;
1; Mismatches
                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MINOR CAPSID PROTEIN L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  670 AA
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                               PRT;
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                                                                                                                                                                                                                                                                                                  PFAM; PF00513; late_protein_L2; 1.
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21-JUL-1986 (Rel. 01, Last sem
                                                                                                                                                                                                                                                                                                                                                           74.48;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 251:191-196(1989).
                                                                                                                                                                                                                                                                            EMBL; U31789; AAA79469.1; -.
                                                                                                                                                                                                                                                                                                               Late protein.
                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 75.0
Matches 6; Conservative
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                               STANDARD;
                                                                                                                                                                                                                                                                                        INTERPRO; IPR000784; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 89325663.
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                                                                                                                                          SEQUENCE FROM N.A.
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43 KIFGSLVY 50
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P00516;
                              VL2_HPV48
Q80925;
                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                  VL2_HPV48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                  -i- SUBUNIT: ANTIPARALLEL HOMODIMER.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND CGK1-BETA (P121136); ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- MISCELLANBOUS: EXHBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK.
                                                                                                                                                protein kinase ";
J. Biol. Chem. 257:727-733(1982).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN.
-!- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME ACTIVATION.
                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CGMP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acetylation; Phosphorylation; Alternative splicing.
"Amino acid sequence around a 'hinge' region and its
'autophosphorylation' site in bovine Lung cGMP-dependent protein
                                                                                                                        Hashimoto E., Takio K., Krebs E.G.; "Amino acid sequence at the ATP-binding site of cGMP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
A8E37ACFE8A7557D CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Pred. No.
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                                                  BIO1. Chem. 258:5531-5536(1983).
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66.78;
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58
101
219
340
618
373
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Best Local Similarity
6; Conserv?
                                                                                      SEQUENCE OF 373-409
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359
365
389
483
670 AA;
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                                                                                                                                                                                                                                                            CDNA cloning and gene expression of human type Ialpha cGMP-dependent
                                                                                30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CCMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1
                                                                                                                                                                                                                                                                                                                                                                                   -i- CATALVIIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
-i- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
ACTIVATION (BY SIMILARITY).
-i- SUBUNIT: ANTIPRABLLEL HOMODIMER (BY SIMILARITY).
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND CGK1-BETA (P14619); ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- MISCELLANBOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-CGMP SUBFAMILY.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 97336057.
Orstavik S., Natarajan V., Tasken K., Jahnsen T., Sandberg M.;
"Characterization of the human gene encoding the type I alpha and
type I beta cGMP-dependent protein kinase (PRKGI).";
Genomics 42:311-318(1997).
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                      MEDLINE; 96188981.
Tamura N., Itoh H., Ogawa Y., Nakagawa O., Harada M., Chun T.,
Suga S., Yoshimasa T., Nakao K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z92867; CAB07436.1; -. FMBL; Z92869; CAB07436.1; JOINED.
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                                                                        (Rel. 39, Created)
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Z92871; CAB07436.1;
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                                                STANDARD;
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                                                                                                                       (CGKI-ALPHA).
                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                    PRKG1 OR PRKGR1A,
                                                                                                                                                                                                                                                                           protein kinase,
                                                                     30-MAY-2000
                                                                                                                                                                                                               TISSUE=LUNG
                                              KGPA_HUMAN
Q13976;
                                                                                                                         ALPHA)
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EMBL;
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                       RESULT
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R INTERPRO; IPRO02373; -.

R INTERPRO; IPRO02373; -.

R INTERPRO; IPRO02373; -.

R PFAM; PF00069; pkinase; 1.

R PFAM; PF00433; pkinase; 1.

R PFAM; PF00431; pkinase; 1.

R PRINTS; PR00109; TYRKINASE.

R PRINTS; PR00100; TYRKINASE.

R PROSITE; PS00100; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00042; CNMP_BINDING_2, 2.

R PROSITE; PS00042; CNMP_BINDING_3; 2.

R PROSITE; PS00042; CNMP_BINDING_3; 2.

R TRANGFARASE; Setine/Chreonine-protein kinase; ATP-binding; CMP-binding; Acetylation; Phosphorylation: Alternative splicing.

T MOD_R PSS SIMILARITY; ACETYLATION (BY SIMILARITY); ATRIBABITY); ATRIBABITY; ATRIBABITY); ATRIBABITY; ATRIBABITY; ATRIBABITY; ATRIBABITY; ATRIBABITY; ATRIBABITY; ATRIBABITY; ATRIBABITY; ATRIBABITY; ATRIBABITY;
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30-MAY-2000 (Rel. 39, Last annotation update)
CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBDNIT: ANTIPRABLEL HOMOTIMER (BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND CGK1-BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-1- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kumar R., Joyner R.W., Lincoln T.M.;
Kumar R., Joyner R.W., Lincoln T.M.;
Kinase in rabbit heart.":
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: APP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
--- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 1; Length 670; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663C4B496F983270 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-NEW ZEALAND WHITE; TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGMP 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequ
30-MAY-2000 (Rel. 39, Last anno
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66.78;
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76233 1
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Best Local Similarity 66.،
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                       IPR002290; -.
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365
389
483
670 AA;
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163 KVFGELAIL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                      42
58
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077676;
INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
MOD_RES
DOMAIN
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SEQUENCE
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KGPA_RABIT
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                            ACETYLATION (BY SIMILARITY).
THTERCHAIN (WITH DIMER) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
DIMERIZATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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0
                                                                                                                                                                                                                                                                                                                                                                     74.4%; Score 32; DB 1; Length 670; 66.7%; Pred. No. 42:
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                                                                                                                                                                                                                                                                                                                                                   CFE1D7D939E1C423 CRC64;
                                                                                                                                                                                                                                                                                                           PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 AA
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1; Mismatches
                                                                                                                                                                                                                                                                                           CGMP 1.
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                                                                                                                                    PFAM; PF00027; cNMP_binding; 2. PFAM; PF00069; pkinase; 1. PFAM; PF00433; pkinase_C; 1.
                                                                     EMBL; AF076969; AAC31192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1991 (Rel. 18, Created)
                                                                                                                                                                                                                                                                                                                                                    76322 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA) (CGKI-BETA).
PRKG1 OR PRKGR1B OR PRKG1B.
                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 60.7.
The 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                     INTERPRO; IPR001245; -.
INTERPRO; IPR002290; -.
INTERPRO; IPR002373; -.
INTERPRO; IPR002374; -.
                                                                                               IPR000961; -.
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58
101
219
340
618
373
                                                                              INTERPRO; IPR000595; - INTERPRO; IPR000719; -
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102
220
359
365
389
483
557
670 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-TESTIS;
MEDLINE; 97256767.
                                                                                                                                                                                                                                                                                                                                                                                                           1 KIFGSLAFL 9
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P21136;
                                                                                                                                                                                                                                                   INIT_MET
MOD_RES
DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                  ACT_SITE
VARIANT
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NP_BIND
NP_BIND
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BINDING
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION.
-!- SUBUNIT: ANTIPARALLEL HONODIMER.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (P00516) AND
CGK1-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
IDENTICAL TO THAT OF CAK.
-!- SIMILARIY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CGMP SUBFAMILY.
Ruth P., Pfeifer A., Kamm S., Klatt P., Dostmann W.R., Hofmann F.; "Identification of the amino acid sequences responsible for high affinity activation of CGMP kinase lalpha."; J. Biol. Chem. 272:10522-10528(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 251:191-196(1989).
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN.
-i- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
                                                                                                                                                                                                                                                                                                                                                                                    Wernet W., Flockerzi V., Hofmann F.; "The CDNA of the two isoforms of bovine cGMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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R EMBL; Y08961; CAA70155.1; -.
R PIR; S05035; S05035.
R INTERPRO; IPR000595; -.
R INTERPRO; IPR000961; -.
R INTERPRO; IPR000961; -.
R INTERPRO; IPR002374; -.
R INTERPRO; IPR002374; -.
R PFAM; PF000433; Dkinase_C; 1.
R PFAM; PF000433; Dkinase_C; 1.
R PRAM; PF000433; Dkinase_C; 1.
R PROSITE; PS000104; CGMPKINASE_ATP; 1.
R PROSITE; PS000104; CGMPKINASE_ATP; 1.
R PROSITE; PS000104; CGMPKINASE_ATP; 1.
R PROSITE; PS000104; CGMPLIN_KINASE_ST; 1.
R PROSITE; PS000108; CNMP_BINDING_2; 2.
R PROSITE; PS000888; CNMP_BINDING_2; 2.
R PROSITE; PS000889; CNMP_BINDING_3; 2.
R PROSITE; PS000889; CNMP_BINDING_3; 2.
R PROSITE; PS000889; CNMP_BINDING_3; 2.
R PROSITE; PS00042; CNMP_BINDING_3; 2.
R PROSITE; PS0042; CNMP_BINDING_3; 2.
R PROSITE; PS0044; R PROSITE; PS044; R
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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1; Mismatches
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                                                                                                                                                                                                                             SEQUENCE OF 1-293 FROM N.A.
TISSUE-TRACHEA SMOOTH MUSCLE;
MEDLINE; 89325663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 66.7
Matches 6; Conservative
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405
499
499
686 AA;
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Maria San

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MIM; 176894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                    "Molecular cloning and predicted full-length amino acid sequence of
the type I beta isozyme of cGMP-dependent protein kinase from human
placenta. Tissue distribution and developmental changes in rat.";
FEBS Lett. 255:321-329(1989).
                                                                                                                                                                                                                                                                                                                                                                     ACTIVATION.

-1 SUBUNIT: ANTIPARALLEL HOMODIMER.

-1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (Q13976) AND CGK1-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1 MISCELLANGOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK.

-1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

-2 GMP SUBFAMILY.

-3 CGMP SUBFAMILY.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 97336057.
Ostavik S., Natarajan V., Tasken K., Jahnsen T., Sandberg M.;
"Characterization of the human gene encoding the type I alpha and
type I beta cGMP-dependent protein kinase (PRKGI).";
Genomics 42:311-318(1997).
                              01-APR-1990 (Rel. 14, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    -i- CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN.
                                                                                                                                                     MEDLINE; 90005998.
Sandberg M., Natarajan V., Ronander I., Kalderon D., Walter U.,
Lohmann S.M., Jahnsen T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
                                                                                                                                                                                                                                                      Sandberg M.;
Submitted (OCT-1989) to the EMBL/GenBank/DDBJ databases.
686 AA
PRT;
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JOINED.
JOINED.
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CAB07437.1; JOINED.
CAB07437.1; JOINED.
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                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequ
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                                                                         PRKG1 OR PRKGR1B OR PRKG1B.
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CAB07437.1;
CAB07437.1;
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CAB07437.1;
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CAB07437.1;
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CAB07437.1;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAB07437.
                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    805702
                                                             BETA) (CGKI-BETA).
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                            TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292868;
292869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P05132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292879;
KGPB_HUMAN
                                                                                                                                                                                                                                            REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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"Cyclic AMP-and cyclic GMP-dependent protein kinases differ in their regulation of cyclic AMP response element-dependent gene transcription.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CGMP-DEPENDENT PROFEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. BLOIL. Chem. 274:8391-8404(1999).
-1- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
-1- ENZYME REGULEATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
ACTIVATION (BY SIMILARRIY).
-1- SUBUNT: ANTIPARALEL HOMODIMER (BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA AND CGK1-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- MISCELLANBOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CARK (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                             PFAM: PF00069; pkinase: 1.

PFAM: PF00069; pkinase: 1.

PFAM: PF0013; cMpb_binding: 2.

PFAM: PF00104; cGMPFINASE.

PROSITE; PS00104; CGMPFINASE_ATP: 1.

PROSITE; PS00109; PROTEIN_KINASE_ATP: 1.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00089; CNMP_BINDING_2: 2.

PROSITE; PS00089; CNMP_BINDING_2: 2.

R PROSITE; PS00089; CNMP_BINDING_3: 2.

R PROSITE: PS00089; CNMP_BINDING_3: 2.

R PROSITE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i - SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE - BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 686;
Pred. No. 43;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A097041AB284F1E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77803 MW;
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STRAIN-C57BL/6; TISSUE-BRAIN;
MEDLINE; 99185054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 66,...
English 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA) (CGKI-BETA).
PRKGI OR PRKGRIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
INTERPRO; IPR000595; -. INTERPRO; IPR000719; -.
                                                                                   INTERPRO; IPR000961; -. INTERPRO; IPR002290; -.
                                                                                                                                                                       INTERPRO; IPR002374; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
236
375
381
405
499
686 AA;
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SEOUENCE
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DOMAIN
NP_BIND
BINDING
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/
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                                                                                                                                                                                 INTERPRO; INTERPRO;
INTERPRO; INTERPRO;
INTERPRO; IPR002.

INTERPRO; IPR002.

PFAM: PF00002; pkinase: 1.

A PFAM: PF00109; pkinase: 1.

A PRINTS; PR00104; CAMKINASE.

DR PRINTS; PR00109; TYRKINASE.

DR PROSITE: PS00108; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00889; CNMP_BINDING_1: 2.

DR PROSITE: PS00889; CNMP_BINDING_3: 2.

DR PROSITE: PS00899; CNMP_BINDING_3: 2.

TRAISferase: Serine/Chreonine-protein kinase; ATP-binding; "GMP-binding; Alternative splicing. CGMP 1 (BY SIMILARITY).

236 427 CCMP 2 (BY SIMILARITY).

ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Odell C., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
--- SIMILARITY: TO YEAST HRC830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 85.7 KDA PROTEIN C1366.03 IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      758 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 43;
1; Mismatches
                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                  EMBL; AF084547; AAD16044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                      NTERPRO; IPR001245; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 KVFGELAIL 187
                                                                                                     MGD; MGI:108174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIFGSLAFL 9
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009782;
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eki T.; All T., Tashiro H., Eki T., All Maliysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Genet. 10:261-268(1995).
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                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last monctation update)
HYPOTHETICAL 117.8 KDA PROTEIN IN STE2-FRS2 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 1029;
Pred. No. 64;
0; Mismatches 2; Indels
                                                                                                                                                                                                       Score 32; DB 1; Length 758;
Pred. No. 47;
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
W; 10B77B212E5AD686 CRC64;
                                                                                                                                                                   FOFE169B570ACC57 CRC64;
                                                                                                                                                                                                                                                                                                                                          PRT; 1029 AA
                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast)
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Σ
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                                                                                                                                                                                                        74.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.4%;
illarity 77.8%;
Conservative
        EMBL; Z54308; CAA91096.1; -. Hypothetical protein; Transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae.";
                                                                                                                                                      753
85645
                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE; 95400292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein;
TRANSMEM 57 77
                                            309
405
5131
513
561
567
667
733
758 AA;
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Best Local Similarity
Matches 7; Conserv
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12 QIFGSILFL 20
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P43571;
                                                                                                     TRANSMEM
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SEQUENCE
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SEQUENCE
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YFC5_YEAST
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1 KIFGSLAFL 9 ||||||| | 826 KIFGSLEIL 834

Oy Dp

Search completed: November 14, 2000, 11:56:11 Job time: 89 sec

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023402 arabidopsis
090485 ceenorhabdi
090412 drosophila
090410 drosophila
090410 drosophila
0904701 xenopus lae
090401 xenopus lae
090401 xenopus lae
090401 xenopus lae
090402 caenorhabdi
07637 dictyosieli
07633 drosophila
020406 drosophila
020407 drosophila
020406 drosophila
030407 drosophila
03040
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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PFAM: PF00757; Furin-11ke; 1.

PFAM: PF01030; Recep_L_domain; 2.

PROSITE; PS00103; FROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

SEQUENCE 1259 AA; 137989 WW; E37364D49C4ACD46 CRC64;
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EMBL, ABO008451; BAA23127.1; -.
HSRP, P00523; 2PTK.
INTERPRO; IPR000494; -.
INTERPRO; IPR0007199; -.
INTERPRO; IPR001245; -.
INTERPRO; IPR001245; -.
INTERPRO; IPR001248; -.
INTERPRO; IPR01248; -.
INTERPRO; IPR01248; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1259 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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689
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044592 caenorhabdi
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020695 caenorhabdi
080113 drosophila
085395 rattus norv
092195 mus musculu
091158 caenorhabdi
095417 caenorhabdi
095417 caenorhabdi
09545 methanopalus
09785 methanopalus
09785 methanobact
092890 chlamydia p
035007 thermotoga
01780 caenorhabdi
091801 caenorhabdi
                                                                                               Search time 18.18 Seconds (without alignments) 46.225 Million cell updates/sec
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                November 14, 2000, 11:54:42
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Listing first 45 summarles
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
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EMBL; AP000005; BAA30241.1; -.
                      Hypothetical
SEQUENCE 50
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Q20695;
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                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Cardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Rershaw J., Kirsten J., Laister N., Latreille P.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Saunders D., Shownkeen R.,
Thlerry Mieg J., Thomas K., Vaudin M., Vaugham K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
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Pred. No. 18;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
Clarke K., Wohldmann P., Harrison M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0390441; AAC4/951.1;
INTERPRO; IPR000168;
INTERPRO; IPR03302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01461; 7tm_4; 1.
NCE 356 AA; 41323 MW; DEF906750193F6A4 CRC64;
                                                                                      Last sequence update)
Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 58.2 KDA PROTEIN PHIL41.
                         356 AA.
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                         PRT;
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                                                           01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2000 (TrEMBLrel. 14, F48G7.1 PROTEIN.
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE: 94150718.
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SEQUENCE
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hiller L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Spreat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                    Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                           Length 502;
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                                                                                                                                                                    Indels
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U40953; AAB52646.1; -.
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120 AA; 14016 MW; B7044AC89DCF2AF8 CRC64;
                         7228A9778B2707B1 CRC64;
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Last annotation update)
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Pred. No. 25;
1; Mismatches
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1 protein.
502 AA; 58165 MW;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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STRAIN-BRISTOL N2;
MEDLINE; 94150718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Miller N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                    :|||||||
123 LFGSLAFL 130
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211 VFGGLAFL 218
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Q92230
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RAY Adman NLD. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Admantides P.G., Scherer S.E. I.I P.M., Hoskins R.A., Galle R.F., Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Bauton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Batton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Batton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazely R.G., Champe M., Pfeiffer B.D., Abril J.F., Agbayani A., Da H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxen E.G., Hell G., Nelson C.R., Millos G.L.G., Abril J.F., Agbayani A., Da H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Bouck J., Brokstein D., Botshakov S., Abril J.F., Agbayani A., Bouck J., Brokstein D., Botshakov S., Abril J.F., Saylan D.A., Butler H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dabhle C., Davenport L.B., Davies P., Andrews Perlos B., Delcher A., Deng Z., Mays A.D., Dew I. Diasse K., Cherry J.M., Cawley S., Dabhle C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dabhle C., Bargen R.C., Ferriaz C., Ferriaz C., Ferriaz C., Ferriaz C., Ferriaz R., Calase R., Gong F., Gorrell J.H., Gu Z., Galan P., Harris M., Andrews P., Lei Y., Levistey D., Helman T.J., Harranger S., Harris M., Andrell B., Modlrac C.D., Krayitz S., Mulp D., Lai Z., Lasko P., Lei Y., Levistey A.A., L.J. J., Li Z., Liang Y., Lin X., Martel B., Moltrech M., Mobarty C., Morris J., Puri V., Mester B., Moltrech M., Murphy B., Murphy L., Muzny D.M., Netlson D.L., Asko P., Lei Y., Levistey A.A., Li J., Li Z., Liang Y., Lin X., Mount S.M., Moy M., Mullshina N., Murphy B., Murphy L., Mussern D., Puri V., Rechert K., Remington K., Sauders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Sturong R., Shue B.C., Siden-Klamos I., Simpson M., Sturong R., Shue B.C., Siden-Klamos I., Simpson M., Sturong R., Shue B.C., Saden-Klamos G.S., Pan S., Pollard W., Wenger E.W., Wenger E.W., Wenley K., Wenger S., Chulp D., Short M., Sho
                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7%; Score 33; DB 5; Length 1760; Best Local Similarity 75.0%; Pred. No. 3.6e+02; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1760 AA; 202782 MW; B8E0602350E87F86 CRC64;
                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PRT; 1760 AA.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                               CG7586 PROTEIN.
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLFACTORY RECEPTOR (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Singer M.S., Hughes T.E., Shepherd G.M., Greer C.A.;
"Isolation of olfactory receptor mRNA sequences from olfactory bulb glomerular layer."
submitted (SEP-1978) to the EMBL/GenBank/DDBJ databases.
EMBL; AF091576; AAC64596.1; -.
INTERPRO; IPR000025; -.
PRAM; PF00001; 7tm.1; 1.
PRINTS; PR00245; OLFARTHODOPSN.
PRINTS; PR00245; OLFARTHODOPSN.
PRNTS; PR00247; GPRRHODOPSN.
PRNTS; PR00247; GLFACTORYR.
                                                                                                                                                                                                                                            Vanderhaeghen P., Schurmans S., Vassart G., Parmentier M.; "Specific repertoire of olfactory receptor genes in the male germ cells of several mammalian species."; Genomics 39:239-246(1997).
EMBL; X89704; CAA61851.1; -.
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NON_TER 157 157
SEQUENCE 157 AA; 17653 MW; 84724899D60CE049 CRC64;
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0-mXY-1999 (TrEMBLrel. 10, Created)
01-MXY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                    Last sequence update)
Last annotation update)
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Pred. No. 70;
157 AA
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                                               01-NOV-1996 (TrEMBLrel. 01, Last sequent 01-JUN-2000 (TrEMBLrel. 14, Last annotal PUTATIVE OLFACTORY RECEPTOR (FRAGMENT).
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                                  Created)
 PRT;
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85.78;
                             01-NOV-1996 (TrEMBLECL. 01,
01-NOV-1996 (TrEMBLECL. 01,
01-JUN-2000 (TrEMBLECL. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00001; 7tm_1; 1.
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Best Local Similarity
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MEDLINE; 97224452.
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Gaps

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Gaps

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Milson R., Angeough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craston M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M., Smith A., Sonnhammer E., Staden R., Saunders D., Shownkeen R. Smaldon N., Smith A., Sonnhammer E., Staden R., Waltson J., Waterston R., Waterston R., Waterston R., Waterston R., Walson A., Welnstock L., Wilkinson-Sproat J., Wohldman P., elegans ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barlow K.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Maieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                              Length 231;
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Pred. No. 1.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                               Nature 368:32-38(1994).
EMBL: 269659; CAA93484.1; -.
SEQUENCE 231 AA; 26252 MW; 1E8271FBE9111A58 CRC64;
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EMBL; X98865: CAB11549.1; -.

INTERPRO; IPROJ01617; -.

PFAM: PF00005: ABC_tran; 1.

SEQUENCE 454 AA; 50540 MW; 222C49339347A70C CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                            Score 32; DB 5;
Pred. No. 73;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       454 AA
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                                                                                                                                                                                                              74.48;
62.58;
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66.78;
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                              Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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SEQUENCE FROM N.A.
MEDLINE; 94150718.
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439 KLFGLLAFV 447
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                                                                                                 elegans.
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Q9VKC2
ID Q9VKC2
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Q9XTU7
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     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                               Krautwurst D., Yau K.W., Reed R.R.; "Identification of ligands for olfactory receptors by functional expression of a receptor library."; call 95:917-926(1999)
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 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steward C.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223
25089 MW; 83097D299076AF5E CRC64;
                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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Last annotation update)
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00245; OLFACTORYR.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
                                                                                                                                                                         223 AA
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   Mismatches
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STRAIN-BL/6; TISSUE-OLFACTORY EPITHELIUM;
MEDLINE; 99091050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.4%; Score 32;
85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                   OLFACTORY RECEPTOR B3 (FRAGMENT).
   Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF102518; AAD13310.1; -. INTERPRO; IPR000276; -. INTERPRO; IPR000725; -.
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   6; Conservative
                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223
223 AA;
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Best Local Similarity
Matches 6; Conserv
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189 FGSLAFM 195
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|189 FGSLAFM 195
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                                                                                                                                                                                                                                             STRUCTURES.
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 Adams W.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Raw Pedicker S.E., Li P.W., Hoskins R.A., Galle R.F., Gaden R.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams W.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Leais S.E., Li P.W., Hoskins R.A., Galle R.F., Sabapara Y.H.C., Palazel R.G., Champe M., Pefelfer B.D., Ram Brandon R.C., Rogers Y.H.C., Helt G., Melson C.R., Miklos G.L.G., Man K.H., Doyle C., Barker E.G., Helt G., Melson C.R., Miklos G.L.G., Man K.H., Doyle C., Barker E.G., Helt G., Melson C.R., Miklos G.L.G., Ram Baradon R.C., Ragardale J., Bayraktaroglu L., Beaslay E.M., Ballew R.M., Basu A., Baxadale J., Bayraktaroglu L., Beaslay E.M., Ballew R.M., Deng E. Workstein P., Brottler P., Carler J., Candre P., Brottler P., Ramider B.E., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Hannel B.E., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Hannel B.E., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Y., Hannel B.E., Kodire C.D., Kraft C., Kravitz S., Kulp D., Brottler P., Shen H., Roultson D.M., Murphy B., Murphy L., Murzhy D.M., Nowy M., Wown R., Mulliams S.M., Woodage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00324; aa_permeases; 1.
SEQUENCE 500 AA; 54820 MW; 48BB44291114FEB8 CRC64;
           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003634; AAF53154.1; -. FLYBASE; FBgn0032403; CG12317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                               SEQUENCE FROM N.A.
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                                                        CG12317 PROTEIN.
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043282;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 12, Last annotation update)
01SULFIDE-ISOMERASE (EC 5.3.4.1) (PROTEIN DISULFIDE ISOMERASE) (S-S
REARRANGASE) (FRAGMENT).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliane (Mouse-ear Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065866; AAC97669.1; SEQUENCE 149 AA: 17849 MW; 867139E34BE87407 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 99102612.
Affonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
"The genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73:533-552(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: REARRANGEMENT OF BOTH INTRACHAIN AND INTERCHAIN DISULFIDE BONDS IN PROTEINS TO FORM THE NATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.1%; Score 31; DB 12; Length 149; 55.6%; Pred. No. 74; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 10; Length 50;
Pred. No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-FLOWER BUDS OF A.THALIANA ECOTYPE COLUMBIA C24;
Mache R., Quigley F., Thomas F., Yu DY.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 AA; 5390 MW; 25DB1455B42FC682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
0RF MSV137 HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 AA.
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Melanoplus sanguinipes entomopoxvirus.
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                            Brassicaceae; Arabidopsis.
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Best Local Similarity 55.6
Matches 5; Conservative
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Search completed: November 14, 2000, 11:55:43 Job time: 61 sec

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RX MEDLINE; 98037514.

RX MEDLINE; 98037514.

RA Aldredge T., Bashirzadah R., Blakely D., Cook R., Gilbert K.,

RA Aldredge T., Bashirzadah R., Blakely D., Cook R., Gilbert K.,

RA Jidredge T., Bashirzadah R., Blakely D., Cook R., Gilbert K.,

RA Jidredge T., Bashirzadah R., Bitt B., Gilbon R.,

RA Jidani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

RA McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,

RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

RT "Complete genome sequence of Methanobacterium thermoautotrophicum

RT "Complete genome sequence of Methanobacterium thermoautotrophicum

RT deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

BRESSOURCE 232 AA: 26259 MW; BBF39317E95A5BED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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STRAIN-CWL029;
MEDLINE; 99206606.
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
BMBL; ARO01596; AAA118254.1; -.
SEQUENCE 264 AA; 30237 MW; 755874E5FD16EDF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.1%; Score 31; DB 2; Length 264; 75.0%; Pred. No. 1.3e+02; Live 1; Mismatches 1; Indels
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                        Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
232 AA.
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                                                                                                 Created)
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PRT;
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                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.1
Best Local Similarity 66.7
Matches 6; Conservative
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    PRELIMINARY;
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                                                                                                                                                                                                                                    CONSERVED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanobacterium.
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9 QIEGOLVFL 17
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Q92980
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Matches
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(CTREW) XWALB BDAY ZIHT

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locusta mig
sarcophaga
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uperoleia
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-I. BIOCHEM. ATS AS INHIBITOR OF PHOSPHOLIPASE A2.

-I. PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF THIS, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND CLEAVAGE OF THE MODIFIED PRECURSOR.

-I. SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.

Antibiotic; Lantibiotic.
                                                                                                                                                                                                                                                                                                      Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J., Raschdorf F., Peter H.H.;
"Duramycins B and C, two new lanthionine containing antibiotics as inhibitors of phospholipase A2. Structural revision of duramycin and cinnamycin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR.
Zimmermann N., Freund S., Fredenhagen A., Jung G.;
Zimmermann N., Freund S., Fredenhagen A., Jung G.;
Solution structure of the lantibiotics duramycin B and C.";
(In) Schneider C.H., Eberles A.N. (eds.);
Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
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P41518
P47733
P41493
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P07496
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D-ALANINE (BONDED TO 19).
D-ABU (AMINOBUTYRIC ACID).
D-ABU (AMINOBUTYRIC ACID).
LYSINOALANINE (BONDED TO 6).
LYSINOALANINE (BONDED TO 6).
ALA-S-CYS (METHYLLANTHIONINE).
ABU-S-CYS (METHYLLANTHIONINE).
0133445E27362F00 CRC64;
                                                                                                       P82028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 1; Length 19;
Pred. No. 1.6e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                        Streptoverticillium sp. (strain R2075).
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae;
Streptoverticillium.
                                                                                                                                                                                                   29, Created)
29, Last sequence update)
33, Last annotation update)
                                                                                                                                   ALIGNMENTS
                           TEMC_RANTE
TEME_RANTE
COXI_THUOB
FIBA_SYNCA
BOL3_MEGPE
BOL5_MEGPE
TKC2_CALVO
LOSK_LOCMI
NSK2_SARBU
                                                                                   PTHP_STRSA.
UP21_UPEIN
                                                                                                        UP22_UPEIN
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illarity 57.1%;
Conservative
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Best Local Similarity
Matches 4; Conserv
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STRUCTURE BY NMR
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Copyright (c) 1993 - 2000
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HHP_THICU
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GR75_CANFA
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Uperoleia inundata (Floodplain toadlet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn M.J., Corbett J.M., Wheeler C.H.; "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins."; Electrophoresis 18:2795-2802(1997).
                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MITOCHONDRIAL STRESS-70 PROTEIN (75 KDA GLUCOSE REGULATED PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - FUNCTION: IMPLICATED IN THE CONTROL OF CELL PROLIFERATIO
CELLULAR AGING. MAY ALSO ACT AS A CHAPERONE.
-i - SUBCELLULAR LOCATION: MITOCHONDRIAL.
-i - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
HSC-2DPAGE; P99502; DOG.
                                                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS-i- MASS SPECTROMETRY: MW-1426; METHOD-FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.2%; Score 19; DB 1; Length 13; 75.0%; Pred. No. 4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UPERIN 5.1.
                                                                  13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AA.
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                                                                                                                                                                                                                                              SEQUENCE, AND MASS SPECTROMETRY.
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                                                                STANDARD;
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Matches 3; Conserv
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SEQUENCE 13 A
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10 VFGS 13
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P82036;
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P99502;
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-1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Vespoidea; Vespidae; Vespinae; Vespa.
                                                                                                                                                                                        Pinus pinaster (Maritime pine).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Coniferopsida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                  proteins.";
Electrophoresis 20:1098-1108(1999).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.6, ITS MW IS: 25 KDA.
                                                                                                                                                                                                                                                                     TISSUE-NEEDLE;
MEDLINE; 99274088.
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yasuhara T., Nakajima T., Erspaer V.;
(In) Sakakibara S. (eds.);
Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N141) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 1; Length 13; Pred. No. 4.7e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 1; Length 7; Pred. No. 8.8e+04;
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13 AA; 1354 MW; 220140365DFE5338 CRC64;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-BEC-1998 (Rel. 37, Last annotation update)
VESPID CHEMOTACTIC PEPTIDE T (VESCP-T).
                                                                                             7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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Best Local Similarity
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Best Local Similarity
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FGPLTEV 13
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1 LYGNLPF 7
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P81675;
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SEQUENCE
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                                                                                                                                                                                                                                                     MEDLINE; 92134266.
Matsumoto S., Fonagy A., Kurihara M., Uchiumi K., Nagamine T.,
Chijimatsu M., Mitsui T.;
"Isolation and primary structure of a novel pheromonotropic
neuropeptide structurally related to leucopyrokinin from the armyworm
larvae. Pseudaletia separata."
Blochem. Blophys. Res. Commun. 182:534-539(1992).
-- FUNCTION: HORMONE THAT CONTROLS SEX PHEROMONE PRODUCTION IN
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                   PHEROMONOTROPIN (PSS-PT).
Pseudaletia separata (Armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Hadeninae; Pseudaletia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The structure of PA48009: the revised structure of duramycin."; J. Antibiot. 43:1421-1430(1990).
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Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.2%; Score 19; DB 1; Length 18; 37.5%; Pred. No. 6.5e+02; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
LANTIBIOTIC DURAMYCIN (LEUCOPEPTIN) (ANTIBIOTIC PA48009).
Score 19; DB 1; Length 14; Pred. No. 5.1e+02; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptoverticillium griseoverticiliatum.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae;
Streptoverticillium.
                                                                                                                                                                                                                                                                                                                                                                                                           18 18 AMIDATION.
18 AA; 2200 MW; DDF3A1B75ACB18FF CRC64;
                                                                                                                                                                                                                                                                                                                                            LARVAE.
-!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY
                                                                                                                                                 (Rel. 22, Last sequence update) (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       PIR. 320647. 320647. INTERPRO. IPRO01484: - PROSITE; PS00539; PYROKININ; 1. PYFOKININ. HORMONE; Neuropeptide; Amidation; Pyrokinin. 18 AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AA.
                                                                                                                    18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND STRUCTURE BY NMR STRAIN-PA-48009;
                                                                                                                                        22, Created)
 44.2%;
ilarity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 3; Conserv
 Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                     01-MAY-1992 (Rel.
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7 KVFENVEF 14
                                                        FILES : : 5 IFGAVVXI 12
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                                           2 IFGSLAFL 9
                                                                                                                                                                                                                                               TISSUE-HEAD;
                                                                                                                                                 01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itazaki H.;
                                                                                                                  PHPT_PSESE
P25271;
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P36504;
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SEQUENCE.
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                                                                                              RESULT 6
PHPT_PSESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DURA_STRGV
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                                                                                                                                      cinnanycin.",
J. Antibiot. 43:1403-1412(1990).

J. Antibiot. 43:1403-1412(1990).

J. Antibiot. 43:1403-1412(1990).

J. Antibiot. 53:103-1412(1990).

J. PTM: MATURATION OF LANTIBLIOTICS INVOLVES THE ENZYMIC CONVERSION OF THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND CLEAVAGE OF THE MODIFIED PRECURSOR.

J. SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.

Antibiotic; Lantibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98163340.

Dunn M.J., Corbett J.M., Wheeler C.H.;

Land the two-dimensional gel electrophoresis database of dog heart proteins.";

Electrophoresis 18:2795-2802(1997).

- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY

CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED

TO BE UBIQUINONE.
MEDLINE; 91107436. Frederich G., Marki F., Marki W., Gruner J., Raschdorf F., Peter H.H.; Raschdorf F. and C. two new lanthionine containing antibiotics as inhibitors of phospholipase A2. Structural revision of duramycin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; NAD; Ublquinone; Flavoprotein; FAD; Mitochondrion. NON_TER 12\, 12\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPEPTIDE CHAIN.
-1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
THIS A COMPONENT OF THE HYDROPHOBIC PROTEIN FRACTION.
-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
HSC-2DPAGE; P54713; DOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
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                                                                                                                                                                                                                                                                                                                                                                                                                   D-ALANINE (BONDED TO 19).
D-ABU (AMINOBUTYRIC ACID).
D-ABU (AMINOBUTYRIC ACID).
LYSINOALANINE (BONDED TO 6).
ABU-S-CYS (METHYLLANTHIONINE).
ALA-S-CYS (LANTHIONINE).
ABU-S-CYS (METHYLLANTHIONINE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 1; Length 19;
Pred. No. 1.1e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.5%; Score 17; DB 1; Length 12; 42.9%; Pred. No. 1.1e+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 42 KDA SUBUNIT (EC 1 (EC 1.6.99.3) (COMPLEX I-42KD) (CI-42KD) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AA
                                                                                                                                                                                                                                                                                                                                                                                                  D-ALANINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.98;
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Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-HEART;
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P54713;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=PLASMA;
MEDLINE; 94147970.
|: | |
7 KLLGGL 12
                                                                                                                                                                                                                                                                                            Neuropeptide.
SEQUENCE 15
                                                                                   01-OCT-1994 (
01-OCT-1994 (
01-NOV-1995 (
                                                                                                                                                                                                                                               migratoria."
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                                                            LMA2_LOCMI
P38497;
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P31935;
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NON_CONS
NON_TER
SEQUENCE
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UPAB_HUMAN
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                                                                                                                                                                                                                                                                                     OSGAG (1984).
-!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
OF NEUTROPHILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSAKA (1985).
-!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata,
Vespoidea, Vespidae, Vespinae, Vespa.
                                                                                                                                                                                                                                    Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vespa xanthoptera (Japanese hornet).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Vespoidea; Vespidae; Vespinae; Vespa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                   (In) Munekata E. (eds.);
Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
Osaka (1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
(In) Izumiya N. (eds.);
Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 1; Length 13;
Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 1; Length 13;
Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                Mast cell degranulation; Chemotaxis; Venom; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mast cell degranulation; Chemotaxis; Venom; Amidation.
MOD_RES 13 13 AMIDATION.
SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;
                                                                                                                                                                                                                                                                                                                           AMIDATION.
C85554365DF9233D CRC64;
                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-EC-1998 (Rel. 37, Last annotation update)
VESPID CHEMOTACTIC PEPTIDE A (VESCP-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VESPID CHEMOTACTIC PEPTIDE X (VESCP-X).
                                                                                     13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 AA.
                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                      39.5%;
50.0%;
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50.0%;
                                                                                                                                                                                                                                                                                                                                   13 AA; 1386 MW;
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Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                     Vespa analis (Hornet)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF NEUTROPHILS.
                     :| || :
3 YGPLAXI 9
        FGSLAFL 9
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7 KLLGGL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KIFGSL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 KIFGSL 6
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                                                                                    CRBL_VESAN
P17233;
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SEQUENCE
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                                                             RESULT 9
CRBL_VESAN
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Gaps
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--- MISCELANBOOUS: ON THE ZD-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.9, ITS MW IS: 41 KDA.
                                                                                                                                                                                                                                                                                                                                                           Paemen L., Schoofs L., Proost P., Decock B., de Loof A.; "Isolation, identification and synthesis of Lom-AG-myotropin II, a novel peptide in the male accessory reproductive glands of Locusta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                          Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha, Acridomorpha, Acridoidea, Acrididae, Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 53) (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 1; Length 16;
Pred. No. 1.5e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA; 1592 MW; 8C80FFF4B41941CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D63C5047818114B2 CRC64;
                                                  Score 17; DB 1; Le
Pred. No. 1.4e+03;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insect Blochem. 21:243-248(1991).
--- FUNCTION: MYOTROPIC PEPTIDE.
--- TISSUE SPECIFICITY: MALE ACCESSORY GLANDS.
  15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%;
ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                 TISSUE-MALE ACCESSORY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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STANDARD;
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                                                                                                                                                                                                                                                                                                        SEQUENCE, AND SYNTHESIS
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Gaps

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Length 13; 0; Indels

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TISSUE-COLEOPTILE;
Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zlvy M., de Vienne D.;
The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 98455825.
Young T. W., Kuhn N.J., Wadeson A., Ward S., Burges D., Cooke G.D.;
"Bacillus subtilis ORF yybQ encodes a manganese-dependent inorganic
pyrophosphatase with distinctive properties: the first of a new class of soluble pyrophosphatase?";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Żea mays (Maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPAC_BACME STANDARD; PRT; 16 AA.
P56948;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MANGANESE-DEPENDENT INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AA; 1485 MW; 2EF9116472A39458 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Le
Pred. No. 2.1e+03;
                                                                                                           Score 16; DB 1;
Pred. No. 2e+03;
2; Mismatches
                                                                                                                                                                                                                                                                                                                   14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.2%; Scor.
100.0%; Pre
0;
                                                                                                       37.2%;
50.0%;
                                                                                                                            Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAIZEDB; 123950; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus megaterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                      :||:
8 VFGA 11
                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||
|8 IFG 10
                                                                                                                                                                                    2 IFGS 5
                                                                                                                                                                                                                                                                                                                 UC18_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IFG 4
                                                                                                                                                                                                                                                                                                                                                                                                                             (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE
                                                                                                                                                                                                                                                                                                                                    P80624;
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PPAC_BACME
                                                                                                                                                                                                                                                                               RESULT 15
UC18_MAIZE
 SEES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.";
Electrophoresis 20.1108(1999).
-!- FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF
PHOTOSYSTEM II (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
(SPOT N179) IS: 5.9, ITS MW IS: 22 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOTOSYSTEM II.
-!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
WITH THE PHOTOSYSTEM II COMPLEX.
                                                                                                                                            01-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
01-wv-1997 (Rel. 35, Last annotation update)
01-wv-1997 (Rel. 35, Last annotation update)
00xGRN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (24 KDA SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
0xCEN-1999 (Rel. 38, Last annotation update)
EVOLVING ENHANCER PROTEIN 2 (OEE2) (23 KDA SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Coniferopsida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                             SEQUENCE.
TASSOR-PROTONEMA;
MEDLINE: 97275459.
Kasten B., Buck F., Nuske J., Reski R.;
Cytokinin affects nuclear- and plastome-encoded energy-converting plastid enzymes.";
Planta 201:261-272(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
TISSUE-NEEDLE;
MEDILINE; 9274088.
Costa P., Plonneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plonion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- INDUCTION: BY LIGHT.
-i- SIMILARITY: TO OTHER OEE2 SUBUNITS.
Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8D2B0D54D7C44DC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16; DB 1; Pred. No. 1.8e+03;
                                                                                                           12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pinus pinaster (Maritime pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 12
12 AA; 1182 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 2; Conserv
 | | | | | | | | 4 FLXLAYL 10
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8 VFGA 11
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                                                                                                       PSP3_PHYPA
P80662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSBP_PINPS
P81668;
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SEQUENCE
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Gaps

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0; Indels

PSBP\_PINPS RESULT

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Length 14;

18 AA.

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Tetrahymena pyriformis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
20-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.149) (20-ALPHA-HSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: 17-ALPHA,20-ALPHA-DIHYDROXYPREGN-4-EN-3-ONE NAD(P)(+) = 17-ALPHA-HYDROXYPROGESTERONE + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                          18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;
                                                                                                                                                                                                                                                                                                            SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROXYPREGNENOLONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMODIMER.
PIR; S40502; S40502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S40502; STORY OXIGOREDICTASE; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94107273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 86067985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEUROPEPTIDE A.
                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of morphine.";
     11 :1:
3 IFATLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                      (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
15 IFG 17
                                                                                                              AHD2_TETPY
P35430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IFG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPA_BOVIN
P15506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                             STRAIN-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 19
NPA_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organisation.";
FEBS Lett. 304.119-123(1992).

-I- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
-I- SUBUNIT: F--TYPE APPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CHLOROPLAST
THYLAKOID MEMBRANE.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92316212. Stokes H.W., Hiller R.G.; Scaramuszi C.D., Stokes H.W., Hiller R.G.; "Characterisation of a chloroplast-encoded secy homologue and atpH from a chromophytic alga. Evidence for a novel chloroplast genome
Microbiology 144:2563-2571(1998).

-!- CATALVTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.

-!- COPACTOR: REQUIRES MANGANESE FOR ITS ACTIVITY.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE PPASE CLASS C FAMILY.
                                                                                                                                                                                                                      ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                              DEC-1992 (Rel. 24, Created)
DEC-1992 (Rel. 24, Last sequence update)
UUL-1999 (Rel. 38, Last annotation update)
SYNTHASE A CHAIN (EC 3.6.1.34) (SUBUNIT IV) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00449; ATPASE_A; PARTIAL.
Hydrogen ion transport; CF(0); Chloroplast; Transmembrane.
                                                                                                                                                                              37.2%; Score 16; DB 1; Length 16; 100.0%; Pred. No. 2.4e+03; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 1; Length 17; Pred. No. 2.6e+03; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
                                                                                                                          16 AA; 1828 MW; 3C0E6735D98B38A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. F313DCE74C23CF2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloropiast.
Eukaryota; Haptophyceae; Pavlovales; Pavlova.
                                                                                                                                                                                                                                                                                                                                                                           17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pavlova lutherii (Monochrysis lutheri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X64731; CAA45996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.2%;
ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MENDEL; 2272; PAVlu;atpI;1.
INTERPRO; IPR000568; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AA; 1753 MW;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                         Hydrolase; Manganese.
                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-DEC-1992 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                         ||||
| S IFG 7
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                                                                                                                                                                                                                                                     2 IFG 4
                                                                                                          NON_TER
SEQUENCE
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TRANSMEM
SEQUENCE
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20-АСРНА НУВКОХУ

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Yang H.-Y.T., Fratta W., Majane E.A., Costa E.; "Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO NEUROPEPTIDE B (AA 5-8) (IDENTICAL). AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
                                                               ;
0
37.2%; Score 16; DB 1; Length 18; 100.0%; Pred. No. 2.7e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EC52DAE1F45CFCFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
-1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
PIR; A24749; A24749.
                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                           18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 18
18 18
18 AA; 1921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide: Amidation.
SIMILAR 15 18
MOD_RES 18 18
SEQUENCE 18 AA; 1921 M
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2 IFGSLA 7

65

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Gaps

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Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakamiya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;
"The structure of ancovenin, a new peptide inhibitor of anglotensin I converting enzyme.":
Tetrahedron Lett. 26:665-668(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
LANTIBIOTIC ANCOVENIN.
Streptomyces sp. (strain A647P-2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                      Naqvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
Joernvall H.;
                                                      "Characterization of hemoglobin from the lizard Uromastix hardwickii.";
                                                                                                                                                                                                                 Score 16; DB 1; Length 19;
Pred. No. 2.8e+03;
3; Mismatches 0; Indels
                                                                                                                                 Heme: Oxygen transport; Respiratory protein; Erythrocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 1; Length 19;
Pred. No. 2.8e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P., Submitted (SEP-1995) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C549197D0A492B07 CRC64;
                                                                                                                                                                            C40AD8EA30019057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
HETEROTROPH-SPECIFIC PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                           19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 AA
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                   FEBS Lett. 162:290-295(1983).
PIR, A05305, A05305.
PIRDERPRO, IPRO00971; -
PROSITE; PS01033; GLOBIN; PARTIAL.
                                                                                                                                                                                                                 37.2%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.2%;
50.0%;
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Best Local Similarity 50.uv,
Tahes 3; Conservative
                                                                                                                                                                                                                 Query Match 37.2
Best Local Similarity 40.0
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Thiobacillus cuprinus.
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[1]
SEQUENCE.
MEDLINE; 84029159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
STRAIN-DSM 5494;
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ID LANC_STRSQ
AC P38655;
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SEQUENCE
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HHP_THICU
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                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Hellanthus annuus (Common sunflower).
Eukaryota: Viridiplantee; Embryophyta: Tracheophyta; Spermatophyta;
Magnollophyta: eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Asteroideae; Hellantheae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 18, East annotation update)
Uromastyx hardwickii (Indian spiny tailed lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Leiolepinae;
                                                                                                                                                                                                                                                                                                                               Belsson F., Gardies A.-M., Teissere M., Ferte N., Noat G., Ann esterase neosynthesized in post germinated sunflower seeds is related to a new family of lipolytic enzymes."; Plant Physiol. Biochem. 35:761-765(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- DEVELOPMENTAL STAGE: POST-GERMINATION.
1- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYTIC ENZYMES.
INTERPRO: IPRO1091; LIPASE_GDSL_SER; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
 Score 16; DB 1; Length Lb;
Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.2%; Score 16; DB 1; Length 18; 100.0%; Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SEED FATTY ACYL-ESTER HYDROLASE (EC 3.1.1.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. RUSTICA / VAR. EUROFLOR; TISSUE-SEED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase: Lipid degradation; Glycoprotein
ACT_SITE 13 13 BY SIMILARITY.
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                                   0;
             37.2%;
80.0%;
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                                      Conservative
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Best Local Similarity
          Ouery Match
Best Local Similarity
Matches 4; Conserv
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                                                            3 FGSLA 7
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IFG 11
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P18992;
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P81098;
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SFAH_HELAN
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                 Brevundimonas.
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-1. GATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
-1. SIMILARTY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
-1. FINTLARTY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
-2. FOROGOGS: MDH; PARTIAL.
OXIGORGUCTASE: Tricarboxylic acid cycle; NAD.
-1- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME. I- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBLOTICS. PIR; A61284; EWSMAN.
Antiblotic; Lantiblotic.
                                                                                                                                                                                                                                                                                                                                                                                                            Brevundimonas diminuta (Pseudomonas diminuta).
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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                                               D-ALANINE.
D-ALANINE (BONDED TO 19).
D-ABU (AMINOBUTYRIC ACID).
D-ABU (AMINOBUTYRIC ACID).
LYSINOALANINE (BONDED TO 6).
ABU-S-CYS (WETHYLLANTHIONINE).
ABU-S-CYS (LANTHIONINE).
F434299E2736286A CRC64;
                                                                                                                                                                                    Score 16; DB 1; Length 19;
Pred. No. 2.8e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Length 19;
Pred. No. 2.8e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 AA; 1709 MW; 3E643277AB542F23 CRC64;
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MDH_BREVE
TO MOH_BREVE
STANDARD; PRT; 19 AA.
C P80543;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DF MALATE DEHYDROGENASE (EC 11.1.37) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                          19 AA
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50.0%;
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity
These 3; Conserv?
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MEDLINE; 97334132.
Charnock C.;
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7 FGPL/TW 12
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P80542;
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SEQUENCE
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hypothetical prote
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chymotrypsin inhib
trypsin inhibitor
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cytochrome P450 AL
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Ig heavy chain DJ
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MUC1 enhancer bind
bphB protein - Com
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protein QA300027 -
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gene RB1 protein -
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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B61597
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plastocyanin - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 15-Mar-1996
C;Accession: PA0004
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
B;Umitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A;Reference number: PA0001
A;Reference number: PA0004
A;Molecule type: Protein
A;Residues: 1-17 < KAM>
A;Residues: 1-17 < KAM>
A;Residues: 1-17 < KAM>
C;Superfamily: plastocyanin
C;Superfamily: plastocyanin
C;Keywords: copper; electron transfer
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Pred. No. 37;
1; Mismatches
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
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hypothetical protein (nifA 5' region) - Rhizoblum leguminosarum (fragment)
C;Species: Rhizoblum leguminosarum
C;Species: Rhizoblum leguminosarum
C;Species: 22-dan-1993 #sequence_revision 22-dan-1993 #text_change 08-Oct-1999
C;Accession: S06964
R;Roelvink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.
Mol. Microbiol. 3, 1411-1447, 1989
A;Title: Nucleotide sequence of the regulatory nifA gene of Rhizoblum leguminosarum P
A;Reference number: S06964; MUID:90136072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ig lambda chain J region - sheep (fragment)
(Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(Spacession: A37933
(Spacession: A37933
(Spacession: A37933
(Spacession: A37933)
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C;Species: Rattus norvegicus (Norway rat)

C;Species: Darul995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C;Accassion: B61597

R;Shimeno, H; Toda, A; Ogata, S; Nagamatsu, A.

Drug Metab. Dispos. 19, 291-297, 1991

A;Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto A;Accession: B61597

A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A;Residues: 1-10 <ROE>
A;Cross-references: EMBL:X17073; NID:g46208; PIDN:CAA34923.1; PID:g809748
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A;Cross-references: GB:M60440; NID:g165946; PIDN:AAA31550.1; PID:g552425
C;Keywords: heterotetramer; lmmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 2; Length 10;
Pred. No. 6.4e+02;
0; Mismatches 2; Indels
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Best Local Similarity 66.7
Matches 4; Conservative
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nes 3; Conservative
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2 MFGGMA 7
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2 VFGS 5
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                                                               C; Species: Manduca sexta (tobacco hornworm)
C; Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Feb-1994
C; Accession: A60365
R; Kanost, M.R.
Insect Blochem. 20, 141-147, 1990
A; Title: Isolation and characterization of four serine proteinase inhibitors (serpins)
A; Reference number: A60365
A; Accession: A60365
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C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: Pr0225
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A; Reference number: Pr0222; MUID: 91108337
A; Reference number: Pr0222; MUID: 91108337
A; Reference number: Pr0225
A; Residues: 1-9 exp.
A; Residues: 1-9 exp.
A; Residues: 1-9 exp.
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: A48839
A;Title: Following a diabetogenic T cell from genesis through pathogenesis.
A;Reference number: A48839
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-16 KAT>
A;Residues: 1-16 KAT>
A;Experimental source: NOD, transgenic, diabetogenic T cell clone BDC2.5
A;Resperimental source: NOD, transgenic, diabetogenic T cell clone BDC2.5
C;Reywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 2; Length 20;
Pred. No. 4.9e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-20 <KAN>
C;Keywords: hemolymph; monomer; serine proteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell receptor alpha chain V-N-J region - mouse (fragment)
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                           trypsin inhibitor - tobacco hornworm (fragment)
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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11 GHLAFI 16
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Aldose 1-epimerase (EC 5.1.3.3) - pig (fragment)
NiAlternate names: mutarotase
Cispecies: sus scrofa domestic pig)
Cibate: 03-Feb-1994 as scrofa domestic pig)
Cibate: 03-Feb-1994 sequence_revision 03-Feb-1994 stext_change 07-May-1999
CiAccession: PU0033
Final Association of Name of Nam
Ig heavy chain DJ region (clone C68-105) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C; Accession: PH1312
R; Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor ly A; Reference number: PH1302; MUID:93094761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pheromonotropin - armyworm (Pseudaletia separata)
C; Species: Pseudaletia separata
C; Species: Pseudaletia separata
C; Species: Bedaletia separata
C; Species: Solution 1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
C; Accession: JSO647
R; Matsumoto, S.; Fonagy, A.; Kurihara, M.; Uchiumi, K.; Nagamine, T.; Chijimatsu, M.; Biochem. Biophys. Res. Commun. 182, 534-539, 1992
A; Title: Isolation and primary structure of a novel pheromonotropic neuropeptide stru A; Reference number: JSO647; MUID:92134266
A; Reference number: JSO647
A; Molocule type: protein
A; Residues: 1-18 cMAT>
C; Reywords: amidated carboxyl end
F; 18/Modified site: amidated carboxyl end (Leu) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 2; Length 17;
Pred. No. 1.1e+03;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-17 <WAS>
C;Keywords: heterotetramer; immunoglobulin
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ilarity 37.58;
Conservative
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Best Local Similarity 60.0°
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
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7 KVFENVEF 14
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Blochem. J. 317, 879-884, 1996
A:Tilte: Characterization of pig liver glutathione S-transferases using HPLC-electrospra
A:Reference number: S71864; MUID:96332484
A:Accession: S71864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A) Experimental source: liver; cytosolic
C; Comment: At least five species independent classes of cytosolic glutathion transferase
S mitochondrial form are known.
C; Complex: dimer
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a A:Pathway: detoxification; xenobiotics metabolism A:Note: Increased hydrophilicity of GSH-conjugates facilitates their further metabolism es of damage
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C:Species: Hordeum vulgare (barley)
C:Species: Hordeum vulgare (barley)
C:Species: Hordeum vulgare (barley)
C:Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2000
C:Accession: 540530
R:Yupsanis, T.; Burgess, S.R.; Jackson, P.J.; Shewry, P.R.
J. Exp. Bot. 41, 385-392, 1990
A:Title: Characterization of the major protein component from aleurone cells of barley A:Accession: 540530
A:Accession: 540530
A:Accession: 540530
A:Accession: preliminary
A:Molecule type: protein
A:Residues: 1-17 < VUD>
C:Superfamily: 91ycinin
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N.Alternate names: glutathione S-transferase class alpha 6a
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
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   Length 14;
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42.9%; Pred. No. 1.1e+03;
tive 2; Mismatches 2;
   DB 2;
9e+02;
   Score 19; DB 2
Pred. No. 9e+02
1; Mismatches
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Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0v
امروم 4; Conservative
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A; Residues: 1-17 <ROU>
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11 VFGPRSF 17
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GSLLF 6
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Indels

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PC4213
PC4213
PC4213
DphB protein - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni
C;Species: Comamonas testosteroni
C;Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 08-Oct-1999
C;Accession: PC4213
R;Sylvastre, M.; Sirois, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Bar Gene 174, 195-202, 1996
A;Title: Sequencing of Comamonas testosteroni strain B-356-biphenyl/chlorobiphenyl di A;Reference number: JC4993; MUID:97045812
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A:Residues: 1-19 <NAR>
R:Residues: 1-19 <NAR>
R:Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A:Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structun A; Reference number: A53359
A;Contents: annotation; strain L337-2
C; Superfamily: cinnamycin precursor.
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C;Accession: A45767

R;Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase, J. Antibiot. 42, 837-845, 1989

A:Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and propertie A;Reference number: A45767; MUID:89291558
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F:1-18/Cross-link: (25,35,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:4-14/Cross-link: Sn-(25,5R)-lanthionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (25,35,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:6-19/Cross-link: (2xi,9S)-lysinoalanine (Ser-Lys) #status experimental
F:15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
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C;Species: Streptoverticillium cinnamoneum
C;Date: 30-Sep-1993 #sequence_revision 12-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:U47637; NID:91245151; PIDN:AAC44530.1; PID:91245156 A;Experimental source: strain B-356 C;Genetics:
                                                  Length 14;
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         Score 18; DB 2; Ler
Pred. No. 1.5e+03;
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Pred. No. 1.6e+03;
3; Mismatches 3;
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Pred. No. 2e+03;
1; Mismatches
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33.3%;
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                                         Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 33.3
Matches 3; Conservative
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Best Local Similarity
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A; Molecule type: DNA
A; Residues: 1-15 <SYL>
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2 KLTGEVALI 10
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7 FGPFTFV 13
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3 QIYGS
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                                                                                                                                                                                                                                                                                                                                            C; Species: Aplysia californica (California sea hare)
C; Species: Aplysia californica (California sea hare)
C; Date: 14.5ep-1990 #sequence_revision 14.5ep-1990 #text_change 24.Jun-1993
C; Accession: A35594
C; Accession: A35594
R; Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R. Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988
A; Title: Structure and action of buccalin: a modulatory neuropeptide localized to an ide A; Reference number: A35594; MUID:88320404
A; Reference number: A35594
A; Accession: A35994
A; Accession: A35594
A; Acc
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C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Sate: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C. Satession: A59018
C. Satession: A59018
C. Species: May 1998
C. May 1998
C. Species: May 
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C;Species: Eptatretus stouti (Pacific hagfish)
C;Species: Botatretus stouti (Pacific hagfish)
C;Species: Botatretus stouti (Pacific hagfish)
C;Accession: B3911
R;Varner, J.: Neame, P.: Litman, G.W.
R;Varner, J.: Neame, P.: Litman, G.W.
Rroc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A:Title: A secum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil A:Reference number: A39111; MUID:91156684
A:Accession: B39111
A:Statuus: preliminary
A:Molecule type: protein
A:Residues: 1-14 < VAR>
C;Keywords: heterotetramer; immunoglobulin
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1.1e+03;
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Pred. No. 1.5e+03;
2; Mismatches 0; Indels
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Live 0; Mismatches
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60.0%;
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7 VFGDL 11
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2 IFGSL 6
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4 SLAF 7
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4 YGNLA 8
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Gaps

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Gaps

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Indels

C; Keywords: T-cell receptor

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peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N.Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FC; Specias: Homo sapiens (man)
C.Specias: Homo sapiens (man)
C.Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C.Accession: B45115
E.Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton J. Biol. Chem. 267, 21751-21760, 1992
A;Title: Characterization of high molecular weight FK-506 binding activities reveals A;Reference number: A45115; MUID:93016131
                                                                                                                                                                                                                                                                                                                  protein QA100006 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0027
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
Submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A;Reference number: PA001
A;Reference number: PA001
A;Residues: 1-15 <KAM>
A;Experimental source: callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein QA300027 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0026
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
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                            Length 12;
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                                                                                 Indels
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                         Score 17; DB 2;
Pred. No. 2e+03;
1; Mismatches
                            39.5%;
57.1%;
Ouery Match
Best Local Similarity 57.1.
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A; Molecule type: protein
A; Residues: 1-15 <KAM>
A; Experimental source: leaf
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5 IVGTEAF 11
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3 KVYG 6
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3 KVYG 6
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                                                                   C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Date: 28-Oct-1997 #sequence_revision: Pc4373
R:Sarlg, G: Weisman-Shomer, P.; Fry, M.
Blochem. Blophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA A:Accession: Pc4373
A:Accession: Pc4373
A:Accession: Pc4373
A:Accession: Pc4373
A:Accession: Pc4373
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular F;1-4/Domain: RNP1 #status predicted <RNNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G:Species: Mus sp. (mouse)
C:Species: Mus sp. (mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
R:Andres, V.: Fisher, S.: Wearsch, P.: Walsh, K.
A:Andres, V.: Fisher, S.: Wearsch, P.: Walsh, K.
A:Antie: Regulation of Gax homeobox gene transcription by a combination of positive fact A:Reference number: A57458
A:Accession: A57458
A:Accession: A57458
A:Residues: preliminary: translated from GB/EMBL/DDBJ
A:Residues: 1-11 cRES>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47393
R;Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A;Reference number: S47355
A;Accession: S47393
A;Accession: S47393
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 < LEH>
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                                                     tetraplex DNA binding protein qTBP42 III - rat (fragment)
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 2; Length 11; Pred. No. 1.8e+03; 1; Mismatches 1; Indels
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C;Genetics:
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2 FGFILF 7
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A. Accession: B45115
A. Stetus: prefulminary
A. Note: sequence extracted from NCB1 backbone (NCBIP:116748)
C. Keywords: cis-trans-isomerase; cyclosporin A binding
Ouery Match
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Best Local Sinilarity 60.0%; Pred. No. 2.5e+03;
C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house house)
C. Species: Musculus (house mouse)
C. Species: Musculus (house house)
C. Species: Musculus (house house)
C. Species: Musculus (house house)
C. Musculus (house house)
C. Species: Musculus (house house)
C. Mus
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Search completed: November 14, 2000, 11:58:05 Job time: 72 sec

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5 SLAFL 9

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097668 equus cabal. 09t2g8 solanum tub 09umm9 homo saplen 073129 human lmmun 091498 pseudomonas 09t2k6 cucurbita m
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Q9uqa5 homo sapien
Q9t2v7 homo sapien
Q9uw4 methanobact
O62810 equus cabal
P92070 euhadra her
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Ogtzh4 spinacia ol
Ogqes tomato yell
Ol6028 homo sapien
Ogtnpi mus sp. mhc
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4 foot-and-mo
paralichthy
 P82394 litoria ran
P82395 litoria ran
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                                                                                    homo sapien
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                                                                                                                                               mycoplasma.
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MEDLINE; 2002299.
Clark M.A., Morran N.A., Baumann P.;
"Sequence evolution in bacterial endosymbionts having extreme base
                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                           09pxe4 1
P92818 pe
077879 or
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1.4e+02;
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Buchnera aphidicola.
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                            18 AA; 1885 MW; 96F90D72D88F4425 CRC64;
                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last annotation update)
01-JUL-1997 (TREMBLrel. 04, Last annotation update)
MAA MOSAIC MERCURY RESISTANCE TRANSPOSABLE ELEMENT
MER-OPERON)1040 BP (FRAGMENT).
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P82394
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P82395
O97668
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O73129
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O97286
O97286
O77879
O19789
O19789
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Mol. Biol. Evol. 16:1586-1598(1999).
EMBL; AF129281; AAF13768.1; -.
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062810
P92070
P82393
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P82391 litoria aur
09707 mus musculu
P82388 litoria aur
P82389 litoria aur
P82392 litoria ran
037710 klebsiella
052837 rhizobium 1
095505 sus scrofa
P8208 litoria gen
090430 human immun
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082403 fragaria ve
P82390 litoria aur
026832 trypanosoma
Q9vv95 drosophila
                                                  Search time 17.04 Seconds (without alignments) 49.317 Million cell updates/sec
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006514 escherichia
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                     297973 seqs, 93374136 residues
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                                                    November 14, 2000, 11:56:53
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
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                                     - protein search, using
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sp_organelle:*
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sp_rodent:*
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bell frogs Litoria aurea and Litoria raniformis.";
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8 KVVGTIAGL 16
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SEQUENCE
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                                                                                                                                     Nikiforov V., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E., Mindlin S., Nikiforov V.;
Intercontinental spread of promiscuous mercury-resistance transposons in environmental bacteria...
Mol. Microbiol. 24:321-329(1997).
EMBL: Y09026; CAA70241.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamstra H.J., Kuipers B., Schijf-Evers D., Loggen H.G., Poolman J.T.; "The purification and protective capacity of Bordetella pertussis outer membrane protelns."; Secuence 13:747-752(1995). SEQUENCE 20 AA; 1874 MW; A41702F66A87C888 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Litoria aurea(Australian frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBRANE PROTEIN (FRAGMENT).
Bordetella pertussis.
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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Pred. No. 6.3e+02;
1; Mismatches 3; Indels.
                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 2; Length 18;
Pred. No. 5.7e+02;
2; Mismatches 1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AUREIN 2.4/2.4.1.
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                                                                                              SEQUENCE FROM N.A.
STRAIN-CH210; TRANSPOSON-TN5059;
MEDLINE; 97303088.
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57.1%;
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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MEDLINE; 96100814.
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3 KLFAALA 9
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P82391;
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Liee J.S., Ishlmoto A., Yanagawa S.i.;
Lee J.S., Ishlmoto A., Yanagawa S.i.;
"Murine leukemia provirus-mediated activation of the Notchl gene leads
to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";
FEBS Lett. 455:276-280(1999).
EMBL, AJ238029; CA840733.1;
NON_TER
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Eur. J. Biochem. 0:0-0(2000).
-!- FUNCTION: AUREIN 2.4 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
Wallace J.C. Tyler M.J.;
"The antiblocits and anticancer aurein peptides from the Australian
bell frogs Litoria aurea and Litoria ranlformis.";
Eur. J. Biochem. 0:0-0(2000).
-!-FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
PEPTIDE 3 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Murldae; Murinae; Mus
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Litoria raniformis, and Litoria aurea (Australian frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylldae;
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Pred. No. 1.2e+03;
2; Mismatches 2; Indels
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1D87980438AAE2F9 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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16 AA; 1630 MW;
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Best Local Similarity 50.0%;
Matches 4; Conservative
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Best Local Similarity 44.4
Matches 4; Conservative
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                                    Amidation; Antibiotic.
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MEDLINE; 90136072.
ROBLVINK P.W., Hontelez J.G.J., Van Kammen A., van den Bos R.C.;
RNocleotide sequence of the regulatory nifA gene of Rhizobium
"Nucleotide sequence of the regulatory infA gene of Rhizobium
leguminosarum PRE: transcriptional control sites and expression in
                                                                                                                                                                                                                                                                                                                                                                           Hoence, S. Schmid M., Dimroth P.;
"Sequence of a gene cluster from Klebsiella pneumoniae encoding malonate decarboxylase and expression of the enzyme in Escherichia
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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Pred. No. 1.6e+03;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
FIXX PROTEIN (10 AA) (FRAGMENT).
              Pred. No. 1.3e+03;
Mismatches 0;
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EMBL; U95087; AAC45462.1; -.
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Mol. Microbiol. 3:1441-1447(1989).
Mol. X17073; CAA34923.1; -.
SEQUENCE 10 AA; 1037 MW; 24A555
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100.0%; Pr
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80.0%;
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01-JAN-1998 (TrEMBLrel. 05,
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01-NOV-1998 (TrEMBLrel. 08,
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4; Conservative
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             Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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9 SIAFL 13
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Wallace J.C., Tyler M.J.;
"The antibiotic and anticancer aurein peptides from the Australian bell frogs Litoria aurea and Litoria raniformis.";
Eur. J. Blochem. 0:0-0(2000).
-:- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
Amidation; Antibiotic.
                                                                                                                                                                                                                                                                                                                              Litoria aurea (Australian frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Pred. No. 1.3e+03;
2; Mismatches 3; Indels
                                                      Ouery Match 46.5%; Score 20; DB 13; Length 16; Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION.
1D9A5DA354DAE2F9 CRC64;
           1D9A5DADB4D240F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION.
1D9A5DADB4DAE2F9 CRC64;
                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AUREIN 2.2/2.2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P82392;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AUREIN 2.5.
                                                                                                                                                                                                                                     16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20;
                                                                                                                                                                                                                                     PRT;
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         1616 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AA; 1616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amidation; Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 4; Conserv
           16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: |:| |
8 KVVGALGSL 16
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13 FGSL 16
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SEQUENCE
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           SEQUENCE
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Litoria.

P82392

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RESULT P82392

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Litoria.

P82389

RESULT 7

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MOD\_RES

095305 095305

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MEDLINE: 87219879.

Etiemble J., Moroy T., Trepo C., Tiollais P., Buendia M.A.;

Etiemble J., Moroy T., Trepo C., Tiollais P., Buendia M.A.;

"Nucleotide sequence of the woodchuck hepatitis virus surface antigen

RNAs and the variability of three overlapping viral genes.";

Gene 500:207-214(1986).

EMBL: MI5594; AAAA69576.1; -.

NON_TER 12

SEQUENCE 12 AA; 1388 MW; 21ABG172F2132B47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=22202V3.1;
Korber B., Van Dyke R., Wolinsky S., Popek E., Macken C., Widmayer Rardequez A., Hansen C., Wiznia A., Luzuriaga K., Viscarello R.; Bardequez A., Hansen C., Wiznia A., Luzuriaga K., Viscarello R.; "The Ariel project: a prospective cohort study of maternal-child transmission of human immunodeficiency virus type 1 in the era of maternal antiretroviral therapy."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AFI12548; AAF13326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.9%; Score 18; DB 12; Length 10; 100.0%; Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA; 961 MW; 4EDD23640DDB1DD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q89243;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
CORE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                   10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08; Pred. wc.
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                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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09T2G9;
01-MAY-2000 (TEMBLEEL 13, 0
01.MAY-2000 (TEMBLEEL 13, 0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Woodchuck hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.0
Matches 4; Conservative
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 !!!
7 KEFGS 11
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SEQUENCE
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Q9T2G9
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                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Litoria genimaculata (Green-eyed tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND MASS SPECTROMETRY .
Rozek T., Waugh R.J., Steinborner S.T., Bowie J.H., Tyler M.J.,
Wallace J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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J. Pept. Sci. 4.111-115(198).
I. INNOCUA: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS.
I. INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMISAND S.UBERIS.
II. TISSUE SPECTROMETRY: SECRETED BY THE SKIN DORSAL GLANDS.
Amphibian skin; Amidation; Antibiotic.
MOD_RES.
18
AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

44.2%; Score 19; DB 13; Length 18;
Best Local Similarity 42.9%; Pred. No. 2.3e+03;
Matches 3; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.2%; Score 19; DB 6; Length 18; 50.0%; Pred. No. 2.3e+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-SMALL INTESTINE;
Winterce A.K., Fredholm M., Davies W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL. 281168; CAB03553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 18 AMIDATION.
18 AA; 1879 MW; 98A1F86BB4FACBBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 18 AA; 1985 MW; 07DBDAC362B0ACD4 CRC64;
                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MACULATIN 2.1.
                                                                                                                                                    18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                    PRELIMINARY;
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1 MFSSVAHL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IFGSLAFL 9
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8 KVAGTIA 14
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4 FGVLKF
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RESULT 12

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P82068

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Gaps

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RESULT 13

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SECUENCE FROM N.A.
MEDLINE: 86278091.
MEDLINE: 86278091.
Brown K.H., brentano S.T., Donelson J.E.;
"Mung bean nuclease cleaves preferentially at the boundaries of variant surface glycoprotein gene transpositions in trypanosome DNA.";
J. Biol. Chem. 261:10352-10358 (1986).
BMBL: MI4020; AAA30305.1;
NON_TER
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
(IATAT 1.2) VARIANT SURFACE GLYCOPROTEIN ELC GENE (FRAGMENT).
Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                              Mallace J.C., Tyler M.J.;
Wallace The Mallace Telegraph of Augustian Strain Strai
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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                                                                                                                                                                                                                                                                                                                     1D9A5DA424DAE2F9 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAY-2000 (TrEMBLrel. 13, Last anno
CG7630 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                             41.9%;
                                                                                                                                                                                                                                                                                                                        SEQUENCE 16 AA; 1616 MW;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.35,
Thes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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4; Conserv
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8 KVVGAIGSL 16
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| LAFL 15
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                                                                                              SEQUENCE.
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Best Local S
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                                                   Litoria.
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Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae;
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                                                                                                                                                                   SEQUENCE.
MEDLINE; 96327808.
Rumeau D., Cuine S., Fina L., Gault N., Nicole M., Peltier G.;
"Subcellular distribution of carbonic anhydrase in Solanum tuberosum
L. Leaves: characterization of two compartment-specific isoforms.";
Planta 199:79-88(1996).
SEQUENCE 15 AA: 1647 MW; CA5B7063CDD32976 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu H., Davis T.M.; "Genetic relationships among Fragaria species based on RAPDs and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) - AN ALDEHYDE OR KETONE
                                              Chloroplast.

Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
U-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AUREIN 2.3.
                                                                                                                                                                                                                                                                                                                                                                                             41.9%; Score 18; DB 8; 80.0%; Pred. No. 3e+03;
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0; Mismatches
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CARBONIC ANHYDRASE (EC 4.2.1.1) (FRAGMENT). Solanum tuberosum (Potato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alcohol dehydrogenase (ADH) gene.";
Genome 0:0-0(1997).
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16 AA; 1666 MW;
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EMBL; AF000215; AAC36542.1;
Oxidoreductase.
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Best Local Similarity
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Matches 3; Conserv
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RIFG 11
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SEQUENCE
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RESULT P82390

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatidas P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gocorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Strong G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelfer B.D., RA Ballew R.M., Basu A., An H.-J., Andrews-Frankoch C., Baldwin D., Ballew R.W., Basu A., Baxendala J., Bayraktarolu L., Beasley E.M., Ballew R.W., Basu A., Baxendala J., Bayraktarolu L., Beasley E.M., Beson K.Y. Benos P.V., Berman B.J., Bhandari D., Bolshakov S., Mortis P. Botchen M.R., Bouck J., Brackstein P., Bolshakov S., Aburtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., Aburtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., Aburtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., Abodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. RA Burtis N.L., Evangelista C.C., Ferraz C., Ferriara S., Pletz S., Dunn P. RA Botlor R., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Abotla M., Month K.J., Evangelista C.C., Ferraz C., Ferriara S., Pletz S., Mann M.P., Hostin D., Housand T.J., Hernandez J.R., Harris M., Alalah E., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jahall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jahall M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jahall M., Malushian N.V., Mobarry C., Morberson D., Merkulov G., Milshian N.V., Mobarry C., Morberson D., Merkulov G., Milshian N., Nobarry C., Morberson D., Randert K., Wenderson W., Plutama G.S., Pan S., Pollard J., Purl, V., Reese M.G., Randers R., Venderson M., Pittema G.S., Pan S., Pollard J., Purl, V., Remington M., Pittema G.S., Pan S., Pollard J., Purl, V., Remington M., Pittema G.S., Pan S., Pollard J., Purl, V., Remington M., Pittema G.S., Pan S., Pollard J., Purl, V., Remington M., Pittema G.S., Pan S., Pollard J., Purl, V., Smith H., Mang C., Siden-Klamos I. Simer-Klamos I. Shapel M., Pollard S., Shapel M., Woll
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AUREIN 3.1/3.1.1/3.1.2.
Litoria raniformis, and Litoria aurea (Australian frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Best Local Similarity
Matches 4; Conserv
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P82394;
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoi
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                         Score 18; DB 13; Length 17; Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 13; Length 17;
Pred. No. 3.4e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                            2; Indels
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Brandon R.B., Glffard J.M., Bell T.K.;

"Isolation of Equine Lactoferrin Gene.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF102025; AAC77463.1; -.

HSSP; P24627; IBLF.
                                 AUREIN 3.1.1.
AUREIN 3.1.2.
AMIDATION.
F6AC17980428EAFD CRC64;
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F6AC0A580428EAFD CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                       1; Mismatches
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(TrEMBLrel. 10, L
(TrEMBLrel. 13, L
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57.1%;
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17
1739 MW;
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Similarity 57.1%;
4; Conservative
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Best Local Similarity کارید
ادم 4; Conservative
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Antibiotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACTOFERRIN (FRAGMENT)
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                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                   17 AA;
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8 KIAGHIA 14
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Search completed: November 14, 2000, 11:57:48
Job time: 55 sec
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Best Local Similarity 100.
Matches 4; Conservative
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STRAIN-SAMPLE P4.25-15;
McDonald D.;
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MEDLINE; 96327808.
RUMeau D., Cuine S., Fina i., Gault N., Nicole M., Peltier G.;
Rumeau D., Cuine S., Fina i., Cault N., Nicole M., Peltier G.;
Subcellular distribution of carbonic anhydrase in Solanum tuberosum
L. leaves: characterization of two compartment-specific isoforms.";
Planta 199:79-88(1996).
SEQUENCE 18 AA: 2017 MW; 5F515AD3CDD3292E CRC64;
                                                    Gaps
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MEDLINE; 91123474.
MEDLINE; 91123474.
TLO M., Mori Y., Olso Y., Saito H.;
"A single base substitution in the coding region for neurophysin II associated with familial central diabetes insipidus.";
J. Clin. Invest. 87:725-728(1991).
EMBL; M63733; AAA69844.1;
NON_TER
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SEQUENCE 19 AA; 1985 MW; 5FF5FCD7BD990451 CRC64;
                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, Asteridae, euasterids I; Solanales,
Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       Score 18; DB 6; Length 18;
Pred. No. 3.6e+03;
2; Mismatches 1; Indels
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80.0%; Pred. No. 3.6e+03;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Solanum tuberosum (Potato).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
ARGININE VASOPRESSIN-NEUROPHYSIN II (FRAGMUNT).
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                        41.9%;
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                    Query Match
Best Local Similarity
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Matches 4; Conserv
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Best Local Similarity
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7 GDVAFV 12
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7 GSKAF 11
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SEQUENCE FROM N.A.
STRAIN=SAMPLE P4.25-15;
Wolinsky S.M., Korber B.T.M., Neumann A.U., Daniels M., Kunstman K.J.,
Whetsell A.J., Cao Y., Ho D.D., Safrit J.T., Koup R.A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases EMBL; U36027; AAA97722.1; -.
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SEQUENCE 19 AA; 2066 MW; E117102D52800EF4 CRC64;
                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                     Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 12; I
Pred. No. 3.8e+03;
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100.0%; Pred. No. ...
19 AA.
                                            Created)
                                                                                                           ENVELOPE GLYCOPROTEIN (FRAGMENT).
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APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                               App
App
Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: DATE:
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION: A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
ANNE: Charlen of charlen of charlen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 43; DB 1; L
100.0%; Pred. No. 1.2e+05;
ive 0; Mismatches 0;
           US-08-485-511A-141
US-08-485-511A-141
US-08-471-913A-141
US-08-487-890A-104
US-08-487-890A-104
US-08-487-9104
US-08-483-577A-104
US-08-483-577A-104
US-08-483-577A-104
PCT-US95-12502-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMNUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6931
TELEEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
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Washington
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CITY: Se
STATE: W
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Search time 12.04 Seconds (without alignments) 12.529 Million cell updates/sec
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/6_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6_COMB.pep:*
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5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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                            Compugen Ltd
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US-08-787-547-70
US-08-486-348A-27
US-08-466-348A-27
US-08-96-516-18
US-08-466-680B-17
US-08-466-680B-17
US-08-466-680B-62
US-08-414-417B-62
US-08-466-680B-62
US-08-466-680B-62
US-08-466-680B-62
US-08-466-680B-36
US-08-467-083-42
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US-08-484-223B-141
US-08-919-597-141
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                                                                                                           November 14, 2000, 11:56:53
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
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length: 20
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Perfect score:
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Sequence 27, Application US/08486348A
Patent No. 5846538
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A. APPLICANT: Chiever, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
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COUNTRY: US

COUNTRY: US

ZIF: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION UNBER: US/08/486,348A

TILING DATE: 07-JUN-1995

TILING DATE: 07-JUN-1995

TILING DATE: 07-JUN-1995
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 31 MAR-1995
CLASSIFICATION: 424
                    6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 1;
Pred. No. 1.2e+05;
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REGISTRATION UNDBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              920010.448C2
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32.629
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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100.0%; Pri
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Best Local Similarity 100..
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amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and I
                                                           Washington
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  ADDRESSEE:
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US-08-414-417B-27
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                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Patent No. 5801005
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                         APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLNG DATE: 22-JAN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08191/003001
                                                                                                                                   Sequence 70, Application US/08787547 Patent No. 5783567 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0810
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7'
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amind acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-787-547-70
                                                                                                                                                                                                                                                                                                                                           1 KIEGSLAFL 9
                    1 KIFGSLAFL 9
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US-08-787-547-70
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Gaps

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Sequence 27, Application US/08466680B
Patent No. 6075122
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/new PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/new ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                               APPLICATE: Soo Hoo, William
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
TITLE OF INVENTION: RESPONSE USING SAME
NUMBER OF SEQUENCES: 50
CORRESPONDECE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
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                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIble OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
    Sequence 18, Application US/08902516 Patent No. 5891432 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-902-516-18
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STATE: Washing
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APPLICANT: Cheever, Martin A.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27, Application US/08468545B Patent No. 5876712 GENERAL INFORMATION:
                                                                                                                                                                                                                      100.0%;
100.0%;
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 100.

Matches 9; Conservative
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CITY: Seattle
STATE: Washington
COUNTRY: US
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-468-545B-27
                                                                                                                                  ; TOPOLOGY:
US-08-486-348A-27
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US-08-902-516-18
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Sequence 62, Application US/08414417B
Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                             APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: POR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083

FILING DATE: 06-JUN 1995

CLASSIFICATION A424

PRIOR APPLICATION NUMBER: US/08/44/417

FILING DATE: 06-JUN 1995

ATPORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REGISTRATION NUMBER: 32,629

REGISTRATION NUMBER: 32,629

REGISTRATION NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFRA: (206) 622-4900

TELEFRA: (206) 622-400
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                        ..
0
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                      Sequence 62, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
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Best Local Similarity الاس،
احد 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 16 amino acids
                                        9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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                                                                                                   1 KIFGSLAFL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-414-417B-62
                                                                                                                                                                                                   US-08-467-083-62
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US-08-467-083-62
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                                        Matches
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PCT-US95-16415-10
Sequence 10, Application PC/TUS9516415
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
TITLE OF INVENTION: CYTOTOXIC T CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 4; Length 9; Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 3;
Pred. No. 1.2e+05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 North Porrey Pines Road, TPC-8
                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 maino acids
TYPE: anino acids
STARNDEDNESS:
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APPLICATION NUMBER: PCT/US95/16415
FILING DATE: 13-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/355,558
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOGGAN, APTIL C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 433.1PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 554-2937
TELEPAX: (619) 554-2937
TELEPAX: 0.000 10:
SEQUENCE CHRRACTERSTICS:
SEQUENCE CHRRACTERSTICS:
06-JUN-1995
06-JUN-1995
08-JUN-1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 amino acids
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                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: La Jolla
STATE: California
COUNTRY: US'
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                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
                                                          FILING DATE: 06
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-466-680B-27
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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: PCR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                             100.0%; Score 43; DB 2; Length 16; 100.0%; Pred. No. 0.0076; Live 0; Mismatches 0; Indels
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COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING ADME: 06-JUN 1995
FILING ADME: 06-JUN 1995
FILING ADME: O6-JUN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920010.448C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 62, Application US/08468545B; Patent No. 5876712; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-6901
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
      TELECOMMUNICATION INFORMATION:
                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62
SEQUENCE CHARACTERISTICS:
LENGTH: 16 anino acid
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.00
--how 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                            ; TOPOLOGY: linear
US-08-486-348A-62
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                                                                                                                                                                                                                                                                                                                                                  1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-468-545B-62
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US-08-468-545B-62
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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Machington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Score 43; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-MAR-1995
CLASSIFICATION: A24
ATORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 32,629
TELECOMMUNICATION INFORMATION:
TELEFAK: (206) 622-4900
TELEFAK: (206) 622-4910
TELEFAK: (206) 622-631
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
TENCTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
NUMBER OF SEQUENCES: 69
CORRESPONDACE ADDRESS:
Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62, Application US/08486348A; Patent No. 5846538; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16 amino acids TYPE: amino acid
                                                                                   CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
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US-08-414-417B-62
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Sequence 36, Application US/08414417B
Patent No. 5801005
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION:
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 1; Length 15; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: JARA-1995
CLASSIFICATION: 424
                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                   PELLCALLO.

FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 5.1 ive 0; Mismatches
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NAME: Sharkey, Richard G.
REGISTRATION UNMER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                              APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
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LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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US-081-36
US-081
                                                                                                                                                           APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCES: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: Gastle
STREET: Washington
COUNTRY: Washington
COUNTRY: US
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100.0%; Pred. No. 0.0076;
"...marrhes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READANCE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/466,680B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
                                               Sequence 62, Application US/08466680B
Patent No. 6075122
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 100.
Matches 9; Conservative
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ZIP: 98104-7092
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KIFGSLAFL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-08-466-680B-62
US-08-466-680B-62
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Gaps

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Indels

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Sequence 36, Application US/08466680B; Patent No. 6075122; GENERAL INFORMATION:
                                                                                                                                        ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15 amino acids TYPE: amino acid
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                                                                            CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/new PROTEIN
TITLE OF INVENTION: POR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TUTLE OF INVENTION: HER-2/new ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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                                                         DB 1; Length 15; 5.1;
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                                                                                                 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 2;
Pred. No. 5.1;
0; Mismatches
                                                         67.4%; Score 29; DB 100.0%; Pred. No. 5.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          Sequence 36, Application US/08486348A; Patent No. 5846538; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/08468545B Patent No. 5876712 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.4%; £ 100.0%;
                                                         Query Match 67.4
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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US-08-414-417B-36
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OWNERS OF SEQUENCES, 69
OWNERS POLICE ADDRESS;
OWNERS OF SEQUENCES AND SERVICE ADDRESS;
OWNERS OF SEQUENCE ADDRESS;
OWNERS OF SEQUENCE ADDRESS;
OWNERS OF SEQUENCE ADDRESS;
OWNERS OF SEQUENCE OF SEQUENCES AND SEQU
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
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TELEFAX: (206) 622-6031
TELEX: 3723836 SEBDANBERRY
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62...
5; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
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ZIP: 98104-7092
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STATE: Washingt
COUNTRY: US
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US-08-414-417B-42
         US-08-467-083-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: BUKOTOXIN GENE FROM PASTEURELLA
TITLE OF INVENTION: SUIS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HATGRAVE, DEVANS & DOYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FURM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34.103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

"NAME OF THE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York
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                                                                                                                                                                                                                                                                                                     67.4%; Score 29; DB 100.0%; Pred. No. 5.1 iive 0; Mismatches
TELEPANE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
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ZIP: 14603
COMPUTER READABLE FORM:
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                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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STRANDEDNESS:
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Best Local Similarity
Matches 5; Conserv
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2 FGSKAF 7
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TOPOLOGY:
US-08-466-680B-36
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Sequence 42, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4.2, Application US/08414417B

Patent No. 5801005

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/new PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: HER-2/new ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPTUTER: IBM PC COMPATIBLE
COMPTUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/POCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   E: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6300 Columbia Center, 701 Fifth Avenue
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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
CORRESPONDENCES: 69
CORRESPONDENCE DIABRESS:
ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42, Application US/08466680B
Patent No. 6075122
GENERAL INFORMATION
APPLICANT: Cheever, Martin A. APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: POR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                             Gaps
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                                     Length 15;
                                                                                             2; Indels
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ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,545B

FILING DATE: 06-JUN-1995

FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Seed and Berry LLP 6300 Columbia Center, 701 Fifth Avenue
                               Score 24; DB 2;
Pred. No. 54;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEFAXE: (206) 622-4900
TELEFAX: (206) 62-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB Pred. No. 54;
                                                                                                                                                                                                                                                                                                RESULT 23
US-08-468-5458-42
; Sequence 42, Application US/08468545B
; Eatent No. 5876712
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%;
62.5%;
                               55.8%;
62.5%;
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Best Local Similarity 62.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
                           Query Match 55.8
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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2 KVLGSGAF 9
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2 KVLGSGAF
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US-08-466-680B-42
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Patent No. 5846538
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disls, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCES: 69
CORRESPONDENCES: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 54;
                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

TELEPHONE:

TELEP
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEG ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Floppy disk
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LENGTH: 15 amino acids
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Best Local Similarity 62.5
Matches 5; Conservative
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STATE: Washington
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2 KVLGSGAF 9
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MEDIUM TYPE:
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Sequence 24, Application US/08237418

Sequence 24, Application US/08237418

Patent No. 5601973

GENERAL INFORMATION:
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
TITLE OF INVENTION: B. and E2

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700

CITY: Washington
STATE: D.C.
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Pred. No. 54;
1; Mismatches 2; Indels
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                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION BATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: SHARKEY, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids

"VOF: amino acids
"VOF: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAECHLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,418
FILING DATE:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/913,613
FILING DATE: 16-JUL-1992
APPLICATION NUMBER: DE P 41 23 760.9
FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.8
Best Local Similarity 62.5
Matches 5; Conservative
      STREET: 6300 CITY: Seattle STATE: Washington COUNTRY: US 7 IP: 9104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C.
USA
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2 KVLGSCAF 9
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REGISTRATION NUMBER: 33,220

REFERENCE/DOCKET NUMBER: 02481-1199-00000

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 202-408-4400

INFORMATION FOR SED ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
TOPOLOGY: linear
US-08-237-418-24

Ouery Match
Best Local Similarity 80.0%; Pred. No. 61;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps
Oy 1 KIFGS 5

I:|||
Db 7 KVFGS 11

Search completed: November 14, 2000, 11:58:19
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(CIASU) NIMALIA BDA9 21HT

us-09-277-074-10.lim20.rag

HLA Class II bindi RR-1 peptide 48 fr RR-1 peptide 49 fr Sequence of VPI ca RR-1 peptide 50 fr RR-1 peptide 51 fr

mela

Tumour homing Mouse B16B15b

r-CGRP-alpha-27-37

Core polypeptide f RF-1 peptide 52 fr Uroplakin tumour a Sequence of Trypsi

Equine influenza v H. influenzae type H. influenzae tran

Human LDL receptor

Chlamydia trachoma Human V3 loop HIV

Fusogenic peptide VLA-4 binding pept

n faec bindi

Chlamydia trachoma Agrobacterium faec HLA class II bindi

Minimum DB Maximum DB

Database

Result

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Searched:

Sequence:

Run on:

Leishmania immunog Cl-protein with mu Rheumatoid arthrit

Fragment of human

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antigen; epitope; immunogenic target protein; PSA; HBVs; HBVs; BPV; HIVI; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1; melanoma antigen; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MRC class I molecule; major histocompatability complex; HIRA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer; algorithm prediction; MBP; CWV; cytomegalovirus; HSV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen fragment 1, from c-ERB2 has binding affinity for HLA-2.1.
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                            W93747
W93317
Y98857
R64603
R64604
P30110
R64605
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Y89178
R64607
Y82864
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Y42730
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Y44796
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93US-0073205.
93US-0159184.
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(first entry)
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                                                            Homo sapiens.
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x_{44444444444448}
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RESULT
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Immunogenic peptid
HER-2/neu syntheti
HER-1/neu protein
HER-2/neu derived
HLA Class I motif
HLA class II bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene 16-enco
Membrane dipeptida
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Amino acid sequenc
                                                                                                  Search time 14.72 Seconds (without alignments) 20.907 Million cell updates/sec
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(SIDSI)gcgdata/geneseq/geneseqp/AA1986.DAT:*
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(SIDSI)gcgdata/geneseq/geneseqp/AA1986.DAT:*
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        268485 seqs, 34193795 residues
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                                                                                                    November 14, 2000, 11:56:53
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Lolium perenne pro Lolium perenne pro Lolium perenne pro Lolium perenne pro

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                          W36824;
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8888888
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                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                             R73685-876 are potential peptide binders of HLA-A2.1 motif. Using motifs disclosed in the invention, these peptides were screened for further motifs. Only peptides with binding affinity of at least 1% (binding affinity is expressed as an IC50 value) as compared to the standard peptide (R71293) in assays. This peptide has an binding value of 0.1500. The peptides of the invention can induce cytocoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate cancer or
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R97507 is a peptide capable of activating cytotoxic T lymphocytes (CTLs) which specifically target malignant cells. The peptide corresponds to amino acids 369-377 of human Her-Z/Neu protein. CTL-activating peptides can be used in a vaccine for protecting against tumour cell formation. CTLs activated by the peptides will lyse tumour cells displaying specific peptides. Antibodies against CTL-activating peptides are useful for the identification of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vivo activation of tumour-specific cytotoxic T lymphocytes - by contacting with polypeptide(s) derived from human p53 or Her-2/Neu
                                                                                                                                                                                                                                                                                                                                                                      ö
                                         Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; malignant cell; antigenic; vaccine; immunisation; activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                     Score 43; DB 15;
Pred. No. 2.1e+05;
Mismatches 0;
                                                                                                     Disclosure; Page 80; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 124; 158pp; English.
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                                                                                                                                                                                                                                                                                                                                     100.0%;
ilarity 100.0%;
Conservative 0;
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                                                                        autoimmune diseases
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           WPI; 1994-302678/37
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                  1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                   Lymphoma, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9618409-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nomo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-DEC-1994;
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                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins
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Synthetic peptides W36824-40 are based on the sequence of the human Her-2/neu protein, wherein each sequence contains the anchor motif for human leukocyte antigen (HLA) A2.1. The present peptide is based on positions 369-377. The ability of these peptides to inhibit the binding of an influenza virus matrix protein peptide MI to HLA A2.1 was measured by inhibition of lysis by an MI specific, HLA A2.1 restricted, cytotoxic T lymphocyte (CTL) clone. The present protein showed 38% inhibition. The peptides were also tested for their ability to elicit an immune response in vivo. However, only H3 (W36824) and H7 (W36826) were able to do this. H3 and H7 peptides are tumour-associated antigens, and were used to immunize a transgenic, non-human vertebrate (that has been modified to express at least one HLA antigen), so that the ailmal produces CTL which displays HLA-restricted T-cell receptor (TCR) specificity for the alpha and beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chains of such TCRs can be amplified from CTLs produced in the above manner. Cells expressing recombinant TCR are used to identify antigens associated with a tumour and to treat tumours in humans. Transgenic mice are a more convenient source of CTL than the tumour-infiltrating lymphocytes previously used. TCR can be humanised to reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Her-2/neu protein; human leukocyte antigen A2.1; HLA; cytotoxic T lymphocyte; CTL; Immune response; tumour-associated antigen; T-cell receptor; TCR; tumour treatment.
similar compounds which may be useful for treating cancer or virally-infected cells, or for diagnosis. The peptide and vaccines produced provide immunity to a high percentage of different ethnic groups, i.e. those with different HIA alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding variable regions of HLA-restricted non-human \tau cell receptor specific for tumour antigen - used to identify tumour antigens and for tumour therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide H3 based on the human Her-2/neu protein.
                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 43; DB 17;
100.0%; Pred, No. 2.1e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 9; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W36824 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0012845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KIFGSLAFL 9
                                                                                                                                                                                                            9 AA;
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W78859 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9831398-A1.
                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    gene therapy
                                                     17-NOV-1998
                                                                                                                                                                                                              22-JAN-1998;
                                                                                                                                                                                                                                  06-JAN-1998;
22-JAN-1997;
                                                                                                                                                                                          23-JUL-1998.
                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The peptide epitope W77119-W77138 were created for human tumour-specific cyctoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific Tmmunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
side-reactions and short peptide derivatives of TCR are more economical to produce than TCR itself, particularly when expressed as a single-chain molecule rather than as a dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disease specific immunogen - comprises disease specific cytotoxic T lymphocyte epitope used to elicit melanoma specific CTL response
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                                                                         Length 9;
                                                                                             Indels
                                                                                                                                                                                                                                                                          Tyrosinase; tyrosinase cytotoxic lymphocyte response; cytotoxic T lymphocyte; cysteine-depleted; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Slingluff CL;
                                                                       100.0%; Score 43; DB 18;
100.0%; Pred. No. 2.1e+05;
Htive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Engelhard VH, Hunt DF, Kittlesen D,
                                                                                                                                                                                                                                                       HER-2/neu synthetic peptide epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 27; 93pp; English.
                                                                                                                                                                                       W77131 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                       98WO-US01592.
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                                                                                                                                                                                                                                (first entry)
                                                                                             Conservative
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                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                               1 KIFGSLAFL 9
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1 kifgslafl 9
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1 kifgslafl 9
                                         9 AA;
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                                                                                                                                                                                                                                                                                                         Synthetic.
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                                          Sequence
                                                                                                                                                                                                            W77131;
                                                                                                                                                                     RESULT
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A microparticle preparation (MP) has been developed, consisting of microparticles having a diameter of less than 100 mu m. The MP comprises:

(a) a polymeric matrix (PM) consisting of one or more synthetic polymers having a solubility in water of less that 1 mg/1; and (b) an expression vector selected from RNA molecules (at least 50% of which are closed circles) or circular plasmid DNA (at least 50% of which are supercoiled). Also described is a MP of at most 20 microns in diameter, comprising: (a) comprising an expression control sequence operatively linked to a coding sequence, where the coding sequence encodes an expression product selected from: (1) a polypeptide at least 7 amino caids in length, having a sequence identical to the sequence of: (1) a fragment of a naturally-occurring mammalian protein: or (ii) a fragment of a maturally-occurring alength and sequence which permits it to command to an MHC class I or II molecule; and (3) the polypeptide or the peptide linked to a trafficking sequence. W69763 to W69765, and W78793 companies of the present invention. The CMPs are highly effective vehicles for the present invention. The CMPs are highly effective vehicles for the present invention. The CMPs are highly effective vehicles for the delivery of polynocleotides interming genetic diseases, infections or tumours or for downregulating
                                                                                                                                                                         Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen; class II associated peptide; pathogen; gene therapy; genetic disease; infection; downregulation; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New preparations of microparticles - comprising a synthetic polymer matrix and nucleic acid comprising an expression vector for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 43; DB 19; Best Local Similarity 100.0%; Pred. No. 2.1e+05; Matches 9; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 10; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Langer RS,
                                                                                    HER-1/neu protein fragment 369-377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US01499
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97US-0787547.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Curley JM, Hedley ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-427556/36.
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RESULT W70057

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The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The method comprises: (a) delivering an antigen to the mammal at a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigen in the mammal's lymphatic system to maintain the immunological CTL response. The method can be used for the delivery of e.g. a differentiation antigen, a tumour-specific multilineage antigen, an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene antigen, or a viral antigen. They can be used for the treatment of disease such as cancer, e.g. malignant melanoma or infectious disease, e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes that is necessary to keep CTL active, cytotoxic and recirculating through the body. Y10071 to Y10639 represent examples of peptide antigens given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inducing a cytotoxic T lymphocyte response - by maintaining a level of antigen in the lymphatic system of a mammal so as to provide a sustained CTL response, used to treat, e.g. AIDS
                                                                                                                                                                                               Cytotoxic T-lymphocyte response, CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
                                                                                                                                                   HLA Class I motif peptide SEQ ID NO:425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 43; 199pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CTLI-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y98846 standard; Peptide; 15 AA.
Y10495 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US14289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0988320.
                                                                                                  (first entry)
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuendig TM, Simard JJL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-120514/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1999
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             WO9902183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1999
                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                 X10495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y98846;
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Y98846
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences shown in W70053 to W70075 represent peptides derived from tER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte antigen (HLA). HLA-A2.1 and are used to exemplify the method of invention of producing antigen-specific cytotoxic T cells (CTLS) in control invention of producing antigen-specific cytotoxic T cells (CTLS) in control invention of producing antigen-specific CTLS (APCS) pretreated with antigen presenting cells (APCS) pretreated with complex (MHC) molecules with antigen presenting cells (APCS) pretreated with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLS. A method for specifically killing carget cells in a human patient is also provided which comprises comparise class I MHC molecules. The pretreated APCS are incubated with the cytotoxic growth factors, thereby producing activated CTLS which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLS composition can then be administered to the patient. The activated CTLS contacting cancers, immune disorders, viral infections, contactions, contactions of the contaction in the contact of the patient. The activated CTLS contaction is a composition or contacting cancers, immune disorders, viral infections, contactions.
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                                                                                                                                                                                          Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of antigen-specific cytotoxic T cells - by incubating immunosent peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen presenting cells
                                                                                                                                              HER-2/neu derived HLA-A2.1 binding peptide 5 (residues 369-377).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                  fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 43; DB 19; Length 9; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Southwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 7; Page 77; 104pp; English.
  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sidney J,
W70057 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US01959
                                                                                             22-OCT-1998 (first entry)
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIM-) EPIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9833888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                   Synthetic
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  Length 9;
                         Indels
100.0%; Score 43; DB 20; 1
100.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 0;
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هال الجارية RESULT Y10495

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(first entry)

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Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes and the secreted polypeptides they encoduseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                      Human gene 16-encoded protein fragment, SEQ ID NO:296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 34; 586pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-106100/09.
                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                W09966041-A1
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22-JUN-1998;
22-JUN-1998;
                                                    19-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-1998;
16-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soppet DR,
Lafleur DW,
                                                                                                                                                                                                                                                                                                                                  23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM,
                                                                                                                                                                                                                                therapy.
     The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitide or peptides y 19812-198319 which are derived from warious antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The created than or equal to 1,000 nM. The pharmaceutical focuses the immune response than or equal to 1,000 nM. The pharmaceutical focuses the immune response covariants selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune control or architical and food at passes of rheumatoid arthritis, multiple sclerosis, and mysathenia gravis), allograft rejection, allergies, lyme disease, hepatitis, or solver interpretation of the peptides of glomerulonephritis and food foot streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides.

Classases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be useful as diagnostic creagents, for example, to determine the susceptibility of an individuals will be at substantial risk of developing chronic infection. The selection of appropriater T and B cell epitopes should allow the cell epitopes of pathogens which are characterized by high sequence epitopes of pathogens which are characterized by high sequence.
                                                Immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allergy; lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.
                                  Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                   New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response
HLA class II binding antigen epitope peptide #35.
                                                                                                                                                                                                                                                                                                                                                  Sidney J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 40; 60pp; English.
                                                                                                                                                                                                                                           99WO-US12066
                                                                                                                                                                                                                                                                            98US-0087192
                                                                                                                                                                                                                                                                                                                                                  Southwood S,
                                                                                                                                                                                                                                                                                                                (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-097143/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 AA;
                                                                                                                                                                                                                                           28-MAY-1999;
                                                                                                                                                                                                                                                                             29-MAY-1998:
                                                                                                                                       Unidentified
                                                                                                                                                                        WO9961916-A1
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Ebner

Wel Y, Young PE, Florence KA; ess GA, Carter KC, Mucenski M,

Endress GA,

Ni J, Rosen CA,

Brewer LA, Olsen HS,

98US-0089507. 98US-0089508. 98US-0089509. 98US-0089510.

98US-0090113

99WO-US13418

Shi Y, Moore PA, Komatsoulis G;

encode,

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Y86215 to Y86333 are the secreted proteins encoded by the 94 human genes.
This sequence represents a fragment of one of the human secreted
This sequence represents a fragment of one of the human secreted
proteins. The genes and their corresponding secreted polypeptides are
useful for preventing, treating or ameliorating medical conditions,
e.g., by protein or gene therapy. Also pathological conditions on
diagnosed by determining the amount of the new polypeptides in a sample
or by determining the presence of mutations in the new genes. Specific
uses are described for each of the 94 genes, based on which tissues they
are most highly expressed in, and include developmental abnormalities
and foctal deficiencies, blood disorders, diseases of the immune system,
autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
disorders, achizophrenia, arthritis, asthma, psoriasis, sepsis, skin
disorders, atherosclerosis, diabetes, cardlovascular disorders, kidney
clisorders, digestive/endocrine disorders, infections and AIDS. The
pollypeptides are also useful for identifying their binding partners.
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Pred. No. 8.3;
; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.48;
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Best Local Similarity
Matches 4; Conserv
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Gaps

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100.0%; Score 43; DB 21; Length 15; 100.0%; Pred. No. 0.009; ive 0; Mismatches 0; Indels

Conservative

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1 KIFGSLAFL 9

Ouery Match Best Local Similarity Matches 9; Conserv

Y86381 standard; peptide; 17 AA.

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RESULT Y86381 ID Y

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The specification describes a method for identifying modulators of a sterol-regulated Site-1 protease. Site-1 protease cleaves sterol regulatory element binding proteins (SREBPS) in the endoplasmic reticulum, initiating release from membranes and activating lipid synthesis. The modulators therefore also modulate cholesterol and fatty acid biosynthesis! The method comprises selecting an agent capable of down regulating Site-1 protease and formulating a composition comprising the agent. The site-1 protease inhibitors are useful for treating a patient for elevated serum cholesterol. Discasses treated include hypercholesterolemia and other lipid metabolism associated conditions. The present sequence was used in the course of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel assay for identifying modulators of sterol-regulated Site-1 protease useful for the treatment of hypercholesterolemia, involves identifying an agent capable of down regulating Site-1 protease activity.
   sterol regulatory element binding protein; SREBP; lipid synthesis; fatty acid biosynthesis; site-1 protease; protease inhibitor; serum cholesterol; hypercholesterolemia; lipid metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 21; Length 16; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldstein Jl.,
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                                                                                                                                           'note "amidated residue"
                                                                                                                                                                             "COOH attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Page 106; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Espenshade PJ,
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y84229 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                 98US-0096571.
99US-0360237.
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62.5%;
                                                                                                                                                                                                                                                                                  99WO-US18544.
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                                                                                                                                                                                                                                                                                                                                                                      (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                      BROWN M S.
CHENG D.
ESPENSHADE P J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                          COLDSTEIN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheng D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-224327/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAWSON R B.
                                                                                                                                                             Misc-difference 16
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Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAKAI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KIFGSLAF 8
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2 kvfrslkf 9
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                                                                                                          Key
Modified-site
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                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sakai J;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (GOLD/)
(RAWS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAKA/)
                                                                                                                                                                                                                                                                                                                                                                                         (BROW/)
                                                                                                                                                                                                                                                                                                                                                                                                        CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                          (ESPE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). V48618 to V49066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological
                                                                                                                                                                                                                         Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulator; sterol-regulated Site-1 protease; cholesterol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                             Membrane dipeptidase-binding ovary homing peptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 20; Le
Pred. No. 2.1e+05;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 152; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y84219 standard; peptide; 16 AA
                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 58.1%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                    Y48923 standard; Peptide; 7
                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US05284
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0042107
99US-0042107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasqualini R,
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-571717/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FGSLAFL 9
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2 vygsmsfl
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   W09946284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1998;
26-FEB-1999;
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                                                                                                                                                         10-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rajotte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conditions
                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                         Y48923;
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                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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Rawson RB;

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Gaps

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Indels

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Antimicrobial peptide fragment from ubiquicidine (residues 1-18).
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                                                                                                                                                                                                                                                                                                                   29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                           29-MAY-1997;
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                                                                                                                                                                                                                                                                            03-DEC-1998
                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Feitsma
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Den
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                                                                                                                                                                                                 Wus sp
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W60420
NO COCOCOCOCO STATES ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a method for identifying modulators of a sterol-regulated Site-1 protease. Site-1 protease cleaves sterol requiatory element binding proteins (SRBBPs) in the endoplasmic reticulum, initiating release from membranes and activating lipid synthesis. The modulators therefore also modulate cholesterol and fatty acid blosynthesis. The method comprises selecting an agent capable of down regulating Site-1 protease and formulating a composition comprising the agent. The site-1 protease inhibitors are useful for relating a patient for elevated serum cholesterol. Diseases treated include hypercholesterolemia and other lipid metabolism associated conditions. The present sequence is derived from site-1 protease, and is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel assay for identifying modulators of sterol-regulated Site-1 protease useful for the treatment of hypercholesterolemia, involves identifying an agent capable of down regulating Site-1 protease
                                                   Modulator; sterol-regulated Site-1 protease; cholesterol; sterol regulatory element binding protein; SREBP; lipid synthesis; fatty acid biosynthesis; site-1 protease; protease inhibitor; serum cholesterol; hypercholesterolemis; lipid metabolism.
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                sequence of a peptide derived from site-1 protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Espenshade PJ, Goldstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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Pred. No. 53;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 24A; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide; 18 AA
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                UNIV TEXAS SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESPENSHADE P J.
GOLDSTEIN J L.
RAWSON R B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown MS, Cheng D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-224327/19.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W95382 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     BROWN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAKAI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KIFGSLAF 8
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2 kvfrslkf
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                                                                                                                                                                        Cricetulus sp
                                                                                                                                                                                                                                                                                              13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                      14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                         23-JUL-1999;
                                                                                                                                                                                                                                                     24-FEB-2000
                acid
                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity
                                                                                                                                                                                                                                                                                                                                                                                                (TEXA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RAWS/)
(SAKA/)
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(GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                 (BROW/)
(CHEN/)
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Ubiquicidine; treatment; diagnosis; prophylaxis; infection; microbial; pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus; Listeria monocytogenes; Gram-negative; Klebsiella pneumoniae; E. coli; enterococcus; Salmonella typhinuriom; Mycobacterium avium; M. fortuitum; fungus; Candida albicans; Cryptococcus neoformens; Aspergillus fumigatis; virus; parasite; Trypanosoma cruzi; Taxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial peptides derived from ublquicidine - useful for prophylaxis, diagnosis and treatment of infections in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour homing peptide; in vivo panning; murine melanoma; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pauwels EKJ;
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60;
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Pred. No. 60;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nibbering PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour homing peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 23; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W60420 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97NL-1006164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barselaar MT;
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AA;
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| kvhgsla 7
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This invention describes nover peptiaces which have anti-tumour, as anti-inflammatory, anti-anglogenic and anti-arthritic activity. Such anti-inflammatory, anti-anglogenic and anti-arthritic activity. Such molecules are identified by treating a purified NGR receptor with a test compound and identifying compounds that bind specifically to the NGR receptor. The peptides of the invention are inhibitors of anglogenesis and can be used to produce conjugates for delivering agents to anglogenesis and can be used to produce conjugates for delivering agents to anglogenic vasculature, particularly anticancer drugs or an imaging agent, for diagnosis or prognosis. These conjugates may be directed to non-tumour convounded tissue, e.g. for treatment of macular degeneration, diabetic retinopathy or rheumatoid arthritis. The peptides provide specific retinopathy or rheumatoid arthritis. The peptides provide specific targeting to tumours, especially their supporting vasculature, since the NGR receptor is exposed to the circulation only in anglogenic vasculature. Precise targeting should reduce the systemic toxicity of anticancer drugs in the conjugates. Complete killing of all target cells may not be essential since partial denudation of endothelium may result in an occlusive thrombus, and endothelial cells are unlikely to become resistant to anticancer agents not to lose the targeting receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGRP; calcitonin-gene-related peptide; rCGRP-alpha; treatment; headache; non-insulin-dependent diabetes mellitus; cardiovascular disease; asthma; skin disease; inflammatory disease; allergic rhinitis; immunoassay; excessive vascular dilation; concomitant reduced tissue blood flow;
                         molecules that home to anglogenic vasculature used as anticancer agents
                                                                                                                                                   This invention describes novel peptides which home to anglogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                morphine tolerance; antibody; diagnostic; neurotransmitter
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                                                                                                  Example VI; Page 115; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Entzeroth M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W93317 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r-CGRP-alpha-27-37 peptide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GSLAFL 9
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                         Identifying
                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                 targets
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W93317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              W60390-432 represent peptides recovered from mouse melaanomas. The peptides are tumour homing peptides, and are identified by in vivo panning. The in vivo panning comprisses administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying a peptide that homes to the tumour, collecting a sample of normal tissue corresponding to the tumour, and determining that the peptide that homes to the tumour is not present in the normal tissue. The tumour homing peptides can be linked to a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour homing peptide; tumour; diagnosis; endothelial cell; melanoma; anglogenic vasculature; anti-tumour; anti-inflammatory; anti-anglogenic; anti-arthitic; NGR receptor; inhibitor; anglogenesis; anticancer drug; prognosis; inflammation; regeneration; wounded tissue; targeting; macular degeneration; diabetic retinopathy; rheumatold arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       Tumour homing molecules and their conjugates - useful for, e g. directing linked molety to tumour containing angiogenic vasculature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 19; Length 7; Pred. No. 2.1e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse B16B15b melanoma derived tumour homing peptide 32.
                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 80; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W93747 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%;
83.3%;
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                                                                        97WO-US16086
                                                                                                                       96US-0710067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occlusive thrombus; murine
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                                                                                                                                                                                                                         Ruoslahti
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                                                                                                                                                                        (BURN-) BURNIIAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                           WPI; 1998-207151/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA;
                                                                                                                                                                                                                         Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasqualini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9913329-A1.
                                                                        10-SEP-1997;
                                                                                                                       10-SEP-1996;
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                       19-MAR-1998
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$\text{SY} \text{SY} \text
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Gaps

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Score 24; DB 20; Length 7; Pred. No. 2.1e+05; Mismatches 1; Indels

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Rist B;

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Synthetic.
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        \mathbf{x} \in \mathbf{H} \times \mathbf{x} \times \mathbf{x} \cup 
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                                                                                                                                                                                                                                                                                                                                                                      The Invention describes peptides derived from calcitonin-gene-related peptide (rGGRP-alpha) (positions 27.37) sequence H-FVPTNVGSEAF-NH2 where (1) 1-3 of the amino acids in the sequence FVPTNVGSE are replaced with K, Y, A, F, P, Hyp, S, L, O, D, H, Acp, Pac, Tic, Hop, Aib, I or G; or (ii) the sequence FVPTNVGS is replaced with NFVPRSKISP, NVAPRSKISP, NVAPTNVGS or ILSSTNVGS and/or (iii) 1-8 of the amino acids in the sequence FVPTNVGSEAF EVPTNVGSE are deleted and (iv) one amino acid in the sequence FVPTNVGSEAF substituted by a protecting group R selected from 3,3-diphenylpropionyl, 2-propylpentanoyl, 3.5-dichlorophenoxyacetyl, 1-adamantylacetyl, 3,5-dibromo-4-hydroxyphenylalanyl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-(4-benzhydryl-1-piperazinyl)-1,5-dloxo-3,3-(tetramethylene)-pentyl or 5,11-dlhydro-6-oxo-6H-dlbenz[b,e]azepin-11-carbonyl. The peptides are useful for treating headache, non-insulin-dependent diabetes mallitus, cardiovascular diseases, skin diseases, inflammatory diseases, alleritus, rinitis, asthma, diseases involving excessive vascular dilation and concomitant reduced tissue blood flow, and morphine tolerance. They are also useful for producing and purifying antibodies, as immunoassay reagents, as diagnostic and analytical tools in neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthitis; multiple sclerosis; myssthenia gravis; AIDS; allograft rejection; allorgy; lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                        Derivatives of calcitonin-gene-related peptide fragment - useful as diagnostic reagents and as CGRP antagonists, for treatment of cardiovascular diseases, headaches and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                   Claim 4; Page 18; 19pp; German
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                                   WPI; 1999-122216/11.
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Best Local Similarity
Matches 5; Conserv
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gslaf 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides y 981812*99339 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The class DR molecules, the pharmaceutical can be used to finduce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune controlled containing pharmaceutical include autoimmune gravis), allograft rejection, allergies, layer disease, hepatitis, coperatoricity, and mysashenia cancer, hepatitis, so the peptide epitopes can be used to enhance immune responses and concerning immunogenic mixtures include prostate cancer, hepatitis, so the peptides may also be used to make monoclonal antibodies useful as potential disgnostic cracinoma, laymphoma, and conditions acuminatum. The peptides may also be used to make monoclonal antibodies useful as diagnostic creagents, for example, to determine the susceptibility of an individual will be at substantial risk of developing chonic infection. The selection of appropriate T and B cell epitopes should allow the categories in all will be at a substantial say and the perfect of evicability and allow and are characterized by high sequence.
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compositions containing immunogenic peptide epitopes for various class II DR molecules useful for inducing helper T cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    __note= "optionally has an amino, acetyl,
9-fluorenylmethoxy-carbonyl, hydrophobic or
macromolecular carrier gp. attached"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variability such as HIV, HCV and Malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                              Claim 1; Page 40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R64603 standard; Pept1de; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.8%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.8
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 kvlgsgaf 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KIFGSLAF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
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55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foot and mouth disease virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83US-0478847.
82US-0368308.
84US-0653475.
84US-0682819.
                             94WO-US05739.
                                                      93US-0073028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BITT/) BITTLE J L.
(SCRI-) SCRIPPS CLINIC & RE.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.000
The 6; Conservative
                                                                                                          Bolognesi DP,
, Wild CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-1992 (first entry)
                                                                                                                                                WPI; 1995-036105/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis.
                                                                                (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1983;
14-APR-1982;
20-SEP-1984;
18-DEC-1984;
                                                                                                                       Petteway SR,
                             07-JUN-1994;
                                                      07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-1983;
  22-DEC-1994
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                                                                                                          Barney SO,
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P30110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                             R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived from respiratory syncitial virus (RSV) (R6450) which have been truncated at the amino terminus. The peptides are DP-178 like peptides. DP-178 like peptides of a size of 3 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions. The peptide defivatives were identified by a computer assisted peptide sequence search. The antivital activity of this peptide is not stated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "optionally has an amino, acetyl, 9-fluorenylmethoxy-carbonyl, hydrophobic or macromolecular carrier gp. attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human immunodeficiency virus; transmembrane protein; gp41; and pha helix; leucine zipper; DP-185; respiratory syncitial virus; RSV.
                                                                                                                                                                                                   search generated synthetic peptides · are inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 16; Length 16;
Pred. No. 85;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                  Matthews TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RF-1 peptide 49 from respiratory syncitial virus.
                                                                                                                                Bolognesi DP, Lambert DM, Wild CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
                                                                                                                                                                                                                                        Claim 14; Page 138; 182pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.8%;
66.7%;
                                                   94WO-US05739
                                                                             93US-0073028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 66.7%
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                                                                                                                                                                       WPI; 1995-036105/05
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                                                                                                        (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                         16 AA;
                                                                                                                                                                                                                transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KIFGSLAFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification.
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                                                   07-JUN-1994;
                                                                                                                                  Barney SO, I
Petteway SR,
                                                                             07-JUN-1993;
WO9428920-A
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                        22-DEC-1994
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                                                                                                                                                                                                   Computer
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R64604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
R64604
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Caps
                                                                                                                                                                                                                                                                                                                                                                                    R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived from respiratory syncitial virus (RSV) (R64590) which have been truncated at the amino terminus. The peptides are DP-1/8 like peptides. DP-1/8 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein 941. It forms a putative alpha helix at the C-terminal end of the 9941 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine Zipper motif. The peptides complex via non-covalent protein interactions. The peptide derivatives were identified by a computer assisted peptide sequence search. The specification.
                                                                                                                                                                                                Computer search generated synthetic peptides - are inhibitors of HIV transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of VPI capisid protein residues 141-160 from the aminoterminus, FMDV, Tubingen type 0, subtype 1, strain Kaufbeuren.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 16; Length 17;
Pred. No. 91;
1; Mismatches 2; Indels
Lambert DM, Matthews TJ;
                                                                                                                                                                                                                                                                                                                     Claim 14; Page 138; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P30110 standard; Protein; 18 AA.
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hydrophob1c
                                                                                                                                                                                                                                                                                                                                                         Gaps
from respiratory syncitial virus (RSV) (R64590) which have been truncated at the amino terminus. The peptides are DP-178 like peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-13 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions. The peptide derivatives were antiviral activity of this peptide is not stated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R64591-623 are peptide derivatives of a 37 mer RP-1 peptide derived from respiratory syncitial virus (RSV) (R64590) which have been truncated at the amino terminus. The peptides are DP-178 like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI; human immunodeficiency virus; transmembrane protein; gp41; alpha helix; leucine zipper; DP-185; respiratory syncitial virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer search generated synthetic peptides - are inhibitors of HIV transmission
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "optionally has a carboxyl, amido, hyd or macromolecular carrier gp. attached
                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matthews TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 from respiratory syncitial virus.
                                                                                                                                                                                                                                                                                                              Score 24; DB 16;
Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lambert DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 138; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R64606 standard; Peptide; 19 AA.
                                                                                                                                                                                                                                                                                                              55.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US05739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolognesi DP,
Wild CT;
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DUKE.
                                                                                                                                                                                                                                                     18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 kingslaft 11
                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                             1 KIFGSLAFL
                                                                                                                                                                                                            specification
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Petteway SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RF-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYDU-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R64606;
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                  The peptides of the invention corresp. to a region on the antigenic Piccenavius capsid protein. The capsid protein FMDV VPI or polio virus VPI. When linked to carriers the peptides are immunogenic. Dose is 20 ug-2mg peptide for inoculations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrophobic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI; human immunodeficiency virus; transmembrane protein; gp41; alpha helix; leucine zipper; DP-185; respiratory syncitial virus;
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                                                                                   Antigenic peptide(s) corresp. to picornavirus capsid protein useful in prodn. of vaccines and in diagnostic tests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macromolecular carrier gp. attached
                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "optionally has an amino, acetyl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9-fluorenylmethoxy-carbonyl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matthews TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RF-1 peptide 50 from respiratory syncitial virus.
                                                                                                                                                                                                                                                                                                                                                    DB 4;
. 96;
                                                                                                                                                                                                                                                                                                                                                  55.8%; Score 24; DB 100.0%; Pred. No. 96; iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                            Disclosure; Page 14; 90pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 138; 182pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R64605 standard; Peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                    Query Match 55.8
Best Local Similarity 100.
Matches 5; Conservative
    Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wild CT;
                                          WPI; 1983-807942/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-036105/05.
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                                                                                                                                                                                                                                                                                         18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
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7 fgsla 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FGSLA 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-1995
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    Bittle JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R64605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
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enhancer fragments at terminal ends and form hybrid polypeptides
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                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.
                                                                                                                                                                                                     Gaps
DP-178 corresponds to amino acids 638 to 673 of the HIV-1
           isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein interactions. The peptide derivatives were identified by a computer assisted peptide sequence search. The antiviral activity of this peptide is not stated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence -
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                                                                                                                                                                         Score 24; DB 16; Length 19;
Pred. No. 1e+02;
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                                                                                                                                                                                                     Indels
                                                                                                                                                                                                    5;
                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Core polypeptide fragment T No. 617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 31; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merutka G,
                                                                                                                                                                                                                                                                                                                       Y89178 standard; peptide; 19 AA.
                                                                                                                                                                         55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US11219.
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                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TRIM-) TRIMERIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-136792/12.
                                                                                                                                                                                    Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                4 kingslafi 12
                                                                                                                                 19 AA;
                                                                                                                                                                                                                              1 KIFGSLAFL 9
                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9959615-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1999
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                                                                                                                                    Sequence
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                   Y89178;
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"optionally has a carboxyl, amido, hydrophobic or macromolecular carrier gp. attached"
                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "optionally has an amino, acetyl,
9-fluorenylmethoxy-carbonyl, hydroghobic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI; human immunodeficiency virus; transmembrane protein; gp41; alpha helix; leucine zipper; DP-185; respiratory syncitial virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer search generated synthetic peptides \boldsymbol{\cdot} are inhibitors of HIV transmission
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                                                                    DB 21; Length 19;
                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RF-1 peptide 52 from respiratory syncitial virus.
                                                                                   1e+02;
                                                                  Score 24; DB 2
Pred. No. 1e+02
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lambert DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 138; 182pp; English.
                                                                                                                                                                                                                                                                                                                                R64607 standard; Peptide; 20 AA.
                                                                  55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US05739
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolognesi DP,
                                                                  Query Match 55.8
Best Local Similarity 66.7
Matches 6; Conservative
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/note-
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                                                                                                                                                                                           19 AA;
                                                                                                                                                                1 KIFGSLAFL 9
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9428920-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barney SO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
Sequence
                                                                                                                                                                                                                                                                                 RESULT 24 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor associated antigen peptides, especially derived from uroplakin, useful as vaccines to prevent or cure cancers including breast, bladder, prostate, pancreas, ovary, thyroid, colon and stomach -
                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fridkin
                                                                                                                                                                                                                                                                                                                                                                                      Tumour associated antigen peptide; TAA; cancer; carcinoma; treatment; prevention; cure; anti-tumour vaccine; metastases; breast; bladder; prostate; pancreas; ovary; thyroid; colon; stomach; carcinoma; MHC Class I; HLA-A2; human; Major Histocompatibility Complex; uroplakin; prostate specific antigen; prostate specific membrane antigen; prostate acid phosphatase; mucin; lactadherin; teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.
                                                                                     ;
0
                                                  Score 24; DB 16; Length 20;
Pred. No. 1.1e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bar-haim E,
                                                                                                                                                                                                                                                                                                                                                        Uroplakin tumour associated antigen (TAA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 104; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD. (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                                                                                                                               Y82864 standard; peptide; 9 AA.
                                                  55.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   981L-0125608.
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                                                                                                                                                                                                                                                                                                                     19-JUN-2000 (first entry)
                                                  Query Match 55.8
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-205463/18.
                                                                                                                                         20 AA;
                                                                                                                        1 KIFGSLAFL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo saptens.
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Sequence
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CC from Lactadherin (BA-46). Those described in records Y82847-Y82854
CC are derived from Mucin and those described in records Y82841-Y82882
CC are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
XX
XX
SQ Sequence 9 AA;

Query Match
Best Local Similarity 71.4%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps
Qy 2 IFGSLAF 8
| | | | | | |
| Db 1 ilgslpf 7

Search completed: November 14, 2000, 11:57:26
Job time: 33 sec
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